

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:39:11 ; Search time 231 Seconds
(without alignment)
494.786 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPIKVGDAIPAVEFEGEP.....VEPDGTGLTCSLAPNISQL 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	214	1	PRDX5_HUMAN
2	830	100.0	214	2	PRDX5_HUMAN
3	822	99.0	215	1	PRDX5_GERAE
4	818	98.6	215	1	PRDX5_PAPHA
5	767	92.4	210	1	PRDX5_MOUSE
6	767	92.4	213	1	PRDX5_RAT
7	763	91.9	213	2	PRDX5_RAT
8	761	91.7	162	2	PRDX5_PIG
9	747	90.0	219	1	PRDX5_BOVIN
10	727	87.6	211	2	PRDX5_MOUSE
11	583.5	70.3	189	2	PRDX5_XENLA
12	536.5	64.6	162	2	PRDX5_BRARE
13	524	63.1	188	2	PRDX5_BRARE
14	494.5	59.6	157	2	PRDX5_ABDAR
15	486.5	58.6	246	2	PRDX5_ABDAR
16	484	58.3	168	2	PRDX5_GLOMR
17	483	58.2	157	2	PRDX5_DROVA
18	481	58.0	190	2	PRDX5_DROVA
19	475.5	57.3	175	2	PRDX5_DROVA
20	408	49.2	89	2	PRDX5_MOUSE
21	400.5	48.3	185	2	PRDX5_PRRU
22	355.5	42.8	184	2	PRDX5_CANAL
23	355.5	42.8	184	2	PRDX5_CANAL
24	354.5	42.7	220	2	PRDX5_CANAL
25	341.5	41.1	167	2	PRDX5_CANAL
26	341.5	41.1	183	2	PRDX5_CANAL
27	337.5	40.7	167	2	PRDX5_CANAL
28	336.5	40.5	188	2	PRDX5_CANAL
29	321	38.7	168	2	PRDX5_CANAL
30	318.5	38.4	185	2	PRDX5_CANAL
31	317	38.2	161	2	PRDX5_CANAL

32	317	38.2	191	2	PRDX5_BRUM
33	314	37.8	161	2	PRDX5_BRUM
34	312.5	37.4	160	2	PRDX5_BRUM
35	310.5	37.4	160	2	PRDX5_BRUM
36	310	37.3	314	2	PRDX5_MAGR
37	309	37.2	197	2	PRDX5_MAGR
38	308.5	37.2	196	2	PRDX5_MAGR
39	308	37.1	157	2	PRDX5_MAGR
40	307.5	37.0	161	2	PRDX5_MAGR
41	307.5	37.0	168	2	PRDX5_MAGR
42	305	36.7	158	2	PRDX5_MAGR
43	304.5	36.7	168	2	PRDX5_MAGR
44	304	36.6	159	2	PRDX5_MAGR
45	303	36.5	161	2	PRDX5_MAGR

ALIGNMENTS

RESULT 1	PRDX5_HUMAN	STANDARD	PRT	214 AA
AC	P30044; Q9UBU5; Q9UBU4; Q9UKX4;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Peroxiredoxin 5, mitochondrial precursor (BC 1.11.1.15) (Pxx-V)			
DE	(Peroxisomal antioxidant enzyme) (Pxx-V)			
DE	(Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOB166)			
DE	(TPX type VI) (Liver tissue 2D-page spot 71B) (Alu corepressor 1).			
GN	Name=PRDX5; Synonyms=ACR1; ORFNames=SB110;			
OS	Homo sapiens (Human).			
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteleostomi; Euteleostomi; Primates; Catarrhini; Hominiidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Kim I.H., Jeong W.,			
RT	"A new type of human thiol peroxidase (human TPX type VI)."			
RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Medline=20145535; PubMed=10679306; DOI=10.1006/birc.2000.2231;			
RT	Zhou Y., Kok K.H., Chun A.C.S., Wong C.M., Wu H.W., Lin M.C.M.,			
RT	"Mouse peroxidase V is a thioredoxin peroxidase that inhibits p53-			
RT	induced apoptosis."			
RL	Biochem. Biophys. Res. Commun. 268:921-927(2000).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.			
RA	Medline=99445545; PubMed=10514471; DOI=10.1074/jbc.274.42.29897;			
RT	Yamashita H., Ayraham S., Jiang S., London R., Van Veldhoven P.P.,			
RT	"Characterization of human and murine PMP20 peroxisomal proteins that			
RT	exhibit antioxidant activity in vitro."			
RL	J. Biol. Chem. 274:29897-29904(1999).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.			
RA	Tissue=lung;			
RT	Medline=99455929; PubMed=10521424; DOI=10.1074/jbc.274.43.30451;			
RT	Knoops B., Clipse A., Bogard C., Arsalane K., Wattiez R., Hermans C.,			
RT	"Cloning and characterization of AOB166, a novel mammalian			
RT	antioxidant enzyme of the peroxidase family."			
RL	J. Biol. Chem. 274:30451-30458(1999).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.			
RA	Medline=20347113; PubMed=10751410; DOI=10.1074/jbc.274.43.30451;			
RT	Seo M.S., Kang S.W., Kim K., Baines I.C., Lee T.H., Rhee S.G.,			
RT	"Identification of a new type of mammalian peroxidase that forms an			
RT	intramolecular disulfide as a reaction intermediate."			
RL	J. Biol. Chem. 275:20346-20354(2000).			

RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99195471; PubMed=10095767;
 RA Kropotov A., Sedova V., Ivanov V., Sazeeva N., Tomlin A.,
 RA Krutikina R., Oel S.L., Griesenbeck J., Buchlow G., Tomlin N.,
 RT "A novel human DNA-binding protein with sequence similarity to a
 RT subfamily of redox proteins which is able to repress RNA-polymerase-
 RT III-driven transcription of the Alu-family retroposons in vitro.";
 RL Eur. J. Biochem. 260:336-346(1999).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Adrenal gland;
 RX MEDLINE=20402571; PubMed=10931946; DOI=10.1073/pnas.160270997;
 RA Hu Z.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
 RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Pu G., Zhang Q.-H.,
 RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Kong R., Ye M., Zhou J.,
 RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
 RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
 RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
 RT axis and full-length cDNA cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Zhang W., Li N., Wan T., Cao X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP PROTEIN SEQUENCE OF 54-63.
 RC TISSUE=Liver;
 RX MEDLINE=93162045; PubMed=1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Paesquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargias R.,
 RA Appel R.D., Hughes G.J.;
 RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:992-1001(1992).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE=21410064; PubMed=11518528; DOI=10.1006/jmbi.2001.4853;
 RA Declercq J.-P., Byrard C., Clippe A., Stricht D.V., Bernard A.,
 RA Knoops B.;
 RT "Crystal structure of human peroxiredoxin 5, a novel type of mammalian
 RT peroxiredoxin at 1.5-A resolution.";
 RL J. Mol. Biol. 311:751-759(2001).
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with
 CC reducing equivalents provided through the thioredoxin system.
 CC Involved in intracellular redox signaling.
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, Mitochondrial (shown here) and
 CC Cytoplasmic+peroxisomal, are produced by alternative initiation;
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC -----
 CC EMBL: AJ249483; CAB62210.1; -; mRNA.
 CC EMBL: AF197952; AAF04856.1; -; mRNA.
 CC EMBL: AF124993; AAF27531.1; -; mRNA.
 CC EMBL: AF110731; AAF03750.1; -; mRNA.
 CC EMBL: AF231705; AAF78899.1; -; mRNA.
 CC EMBL: AF112212; AAF17200.1; -; mRNA.
 CC EMBL: AF242525; AAF9605.1; -; mRNA.
 CC PDB: 1H40; X-ray; A/B/C/D/E/F/G/H=54-214.
 CC PDB: 1HD2; X-ray; A=54-214.
 CC PDB: 1OC3; X-ray; A/B/C=54-214.
 CC PDB: 1URM; X-ray; A=54-214.

DR SWISS-2DPAGE; P30044; HUMAN.
 DR OGP: P30044; -;
 DR EMBL: ENSG00000126432; Homo sapiens.
 DR H-INVDB: HIX0021287; -;
 DR MIM: 606583; -;
 DR GO: GO:0005739; C:mitochondrion; TAS.
 DR GO: GO:0005777; C:peroxisome; TAS.
 DR GO: GO:0005489; F:electron transporter activity; TAS.
 DR GO: GO:0006954; P:inflammatory response; TAS.
 DR GO: GO:0007585; P:respiratory gaseous exchange; TAS.
 DR GO: GO:0006979; P:response to oxidative stress; TAS.
 DR InterPro: IPR000866; AtpC-TSA.
 DR InterPro: IPR012336; Thioredoxin-like.
 DR InterPro: IPR012335; Thioredoxin_fold.
 DR Pfam: PF00578; AtpC-TSA; 1.
 DR 3D-structure; Alternative initiation; Antioxidant;
 DR Direct protein sequencing; Mitochondrion; Oxidoreductase; Peroxidase;
 DR Peroxisome; Polymorphism; Redox-active center; Transil peptide.
 DR TRANSIT 1
 DR INT MET 53 53
 DR CHAIN 54 214
 DR CHAIN ? 214
 DR MOTIF 212 214
 DR DISULFID 100 204
 DR VARIANT 141 141
 DR MUTAGEN 100 100
 DR MUTAGEN 125 125
 DR MUTAGEN 204 204
 DR TURN 58 59
 DR STRAND 61 61
 DR STRAND 66 68
 DR TURN 72 73
 DR STRAND 75 77
 DR HELIX 78 81
 DR TURN 82 84
 DR STRAND 86 92
 DR TURN 95 96
 DR HELIX 98 102
 DR TURN 103 103
 DR HELIX 104 110
 DR TURN 111 111
 DR HELIX 112 116
 DR TURN 117 119
 DR STRAND 122 127
 DR HELIX 131 140
 DR TURN 141 142
 DR TURN 144 146
 DR STRAND 148 151
 DR TURN 153 154
 DR HELIX 156 161
 DR TURN 162 162
 DR STRAND 164 164
 DR TURN 168 169
 DR HELIX 170 173
 DR STRAND 178 178
 DR STRAND 181 186
 DR TURN 187 188
 DR STRAND 189 195
 DR TURN 197 198
 DR TURN 204 205
 DR HELIX 207 214
 DR SEQUENCE 214 AA; 22026 MW; 2FF211210809823E CRC64;
 DR
 DR Query Match 100.0%; Score 830; DB 1; Length 214;
 DR Best Local Similarity 100.0%; Pred. No. 9.56-66;
 DR Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR
 DR 1 MAPIRVGAIPAVEVEFEGEPGNKVNIAELFKGKGVLFQVPGAFTPGCSKTHLPQVEQA 60
 DR |||||

Db 53 MAPIKVGDALPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGAFPTGCKSTHLPGFVBOA 112
 QY 61 EALRAKGVQVVAACSVNDAFTVGEWGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
 Db 113 EALRAKGVQVVAACSVNDAFTVGEWGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172
 QY 121 FGNRLKRFMSWVODGIVKALNVEPDGTGLTCSLAPNIISOL 162
 Db 173 FGNRLKRFMSWVODGIVKALNVEPDGTGLTCSLAPNIISOL 214

RESULT 2

OGIAF2 HUMAN
 ID OGIAF2 HUMAN PRELIMINARY; PRT; 214 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE PRDX5 protein.
 GN Name=PRDX5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 DR EMBL; CRA57203; CAC33484.1; -; mRNA.
 DR SMR; OGIAF2; 54-214.
 DR Ensembl; ENSG00000126432; Homo sapiens.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.
 SQ SEQUENCE 214 AA; 22026 MW; 2PR21121080923E CRC64;

Query Match 100.0%; Score 830; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 9.5e-66;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGAFPTGCKSTHLPGFVBOA 60
 Db 53 MAPIKVGDALPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGAFPTGCKSTHLPGFVBOA 112
 QY 61 EALRAKGVQVVAACSVNDAFTVGEWGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
 Db 113 EALRAKGVQVVAACSVNDAFTVGEWGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172
 QY 121 FGNRLKRFMSWVODGIVKALNVEPDGTGLTCSLAPNIISOL 162
 Db 173 FGNRLKRFMSWVODGIVKALNVEPDGTGLTCSLAPNIISOL 214

RESULT 3

PRDX5 CERAE
 ID PRDX5 CERAE STANDARD; PRT; 215 AA.

AC OGGLW7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Peroxiredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)
 DE (Thioredoxin reductase).
 GN Name=PRDX5;
 OS Cercopithecus aethiops (Green monkey) (Griwet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Cercopithecus.
 NCBI_TaxID=9534;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Knops B., Cheif H.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyi hydroperoxides with
 CC reducing equivalents provided through the thioredoxin system.
 CC Involved in intracellular redox signalling (By similarity).
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic
 CC (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, Mitochondrial (shown here) and
 CC Cytoplasmic+peroxisomal, are produced by alternative initiation;
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----

DR EMBL; AF110736; AAG13453.2; -; mRNA.
 DR HSSP; P30044; 1HD2.
 DR SMR; OGGLW7; 55-215.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;
 KW Peroxidase; Peroxisome; Redox-active center; Transil peptide.
 FT TRANSIT 1 ?
 FT 54 54 Mitochondrion (potential).
 FT INTR_MET 54 54 For isoform Cytoplasmic+peroxisomal.
 FT CHAIN 55 215 Peroxiredoxin 5, isoform Cytoplasmic+peroxisomal.
 FT CHAIN ? 215 Cytoplasmic+peroxisomal.
 FT MOTIF 213 215 Peroxiredoxin 5, isoform Mitochondrial.
 FT MOTIF 213 215 Microbody targeting signal (By
 FT similarity). (By similarity).
 FT DISULFID 101 205 Redox-active (By similarity).
 SQ SEQUENCE 215 AA; 22237 MW; 7C9B45C1B9517B78 CRC64;

Query Match 99.0%; Score 822; DB 1; Length 215;
 Best Local Similarity 98.8%; Pred. No. 4.9e-65;
 Matches 160; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGAFPTGCKSTHLPGFVBOA 60
 Db 54 MAPIKVGDALPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGAFPTGCKSTHLPGFVBOA 113
 QY 61 EALRAKGVQVVAACSVNDAFTVGEWGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
 Db 114 EALRAKGVQVVAACSVNDAFTVGEWGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 173
 QY 121 FGNRLKRFMSWVODGIVKALNVEPDGTGLTCSLAPNIISOL 162
 Db 174 FGNRLKRFMSWVODGIVKALNVEPDGTGLTCSLAPNIISOL 215

RESULT 4

PRDX5 PAPHA
 ID PRDX5 PAPHA STANDARD; PRT; 215 AA.

AC OGGLW7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Peroxiredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)
 DE (Thioredoxin reductase).
 GN Name=PRDX5;
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Papio.

OX NCBI_TaxID=9557;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RA Knoops B., Cherif H.;
 RT "Cloning and characterization of baboon AOEB166/PDX5.";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBA databases.
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with
 CC reducing equivalents provided through the thioredoxin system.
 CC Involved in intracellular redox signaling (By similarity).
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic
 CC (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative initiation;
 CC Comment-2 isoforms, Mitochondrial (shown here) and
 CC Cytoplasmic-peroxisomal, are produced by alternative initiation;
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AF10734; AAC13451.2; -; mRNA.
 CC HSSP: P30044; 1HD2.
 CC SMR: O9GLM9; 55-215.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR InterPro: IPR012336; Thioredoxin-like.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 DR Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;
 KM Peroxidase; Peroxisome; Redox-active center; Transil peptide.
 FT TRANSIT 1 ? Mitochondrion (potential).
 FT INIT MET 54 54 For isoform Cytoplasmic+peroxisomal.
 FT CHAIN 55 215 Peroxiredoxin 5, isoform
 FT Cytoplasmic+peroxisomal.
 FT CHAIN ? 215 Microbody targeting signal (By
 FT MOTIF 213 215 similarity).
 FT DISULFID 101 205 Redox-active (By similarity).
 FT SEQUENCE 215 AA; 22166 MW; 65183A24535C1617 CRC64;
 SQ
 Best Match 98.6%; Score 818; DB 1; Length 215;
 Query Local Similarity 98.1%; Pred. No. 1,le-64;
 Matches 159; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAPIKVGDALPAVEVEGEPGNKVNLAELFKGKGVLFVPGAFPTGCSKTHLPGFVEQA 60
 DB 54 MAPIKVGDALPAVEVEGEPGNKVNLAELFKGKGVLFVPGAFPTGCSKTHLPGFVEQA 113
 QY 61 EALKAGVGVVACLSVNDAAFVTGEMGRARAKREKRVLLADPTGAFKERTDLLLDSLVSI 120
 DB 114 EALKAGVGVVACLSVNDAAFVTGEMGRARAKREKRVLLADPTGAFKERTDLLLDSLVSI 173
 QY 121 FGNRRLRKFSMVVQDGIIVKALNVDPGTGLTSLAFNIISQL 162
 DB 174 FGNRRLRKFSMVVQDGIIVKALNVDPGTGLTSLAFNIISQL 215
 RESULT 5
 PRDX5 MOUSE STANDARD; PRT; 210 AA.
 ID PRDX5_MOUSE
 AC P99029; O9QK45; O9QK75;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Peroxisomal oxidant precursor (EC 1.11.1.15) (Prx-V)
 DE (Thioredoxin peroxidase) (Prp) (Thioredoxin reductase)
 DE (Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOEB166)
 DE (Liver tissue 2D-page spot 2D-00141V).
 GN Name=Prdx5; Synonym=Prdx6;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RN NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
 RP MEDLINE=20145535; PubMed=10679306; DOI=10.1006/birc.2000.2231;
 RA Zhou Y., Kok K.H., Chun A.C.S., Wong C.M., Wu H.W., Lin M.C.M.,
 RA Pung P.C.W., Kung H.-F., Jin D.-Y.;
 RT "Mouse peroxiredoxin V is a thioredoxin peroxidase that inhibits p53-
 RT induced apoptosis.";
 RT Biochem. Biophys. Res. Commun. 268:921-927(2000).
 RN [2]
 RN NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
 RP MEDLINE=99445545; PubMed=10514471; DOI=10.1074/jbc.274.42.29897;
 RA Yamashita H., Avraham S., Jiang S., London R., Van Veldhoven P.P.,
 RA Subramani S., Rogers R.A., Avraham H.;
 RT "Characterization of human and murine PMP20 peroxisomal proteins that
 RT exhibit antioxidant activity in vitro.";
 RT J. Biol. Chem. 274:29897-29904(1999).
 RN [3]
 RN NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=C3H/HeJ; TISSUE=Lung;
 RX MEDLINE=99452929; PubMed=10521424; DOI=10.1074/jbc.274.43.30451;
 RA Knoops B., Clippe A., Bogard C., Arsalane K., Wattiez R., Hermans C.,
 RA Duconcelle E., Falmagne P., Bernard A.;
 RT "Cloning and characterization of AOEB166, a novel mammalian
 RT antioxidant enzyme of the peroxiredoxin family.";
 RT J. Biol. Chem. 274:30451-30458(1999).
 RN [4]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20218665; PubMed=10753630; DOI=10.1006/birc.2000.2430;
 RA Lee T.H., Kim S.J., Kang S.W., Lee K.K., Rhee S.G., Yu D.Y.;
 RT "Molecular cloning and characterization of the mouse Peroxiredoxin V
 RT gene.";
 RT Biochem. Biophys. Res. Commun. 270:356-362(2000).
 RN [5]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=1246651; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamashita H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brade D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmig L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shireki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Jehli Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RT Nature 420:563-573(2002).
 RN [6]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Mammary tumor;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H.
1, R.R.; Melalano, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82051
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <HE>
A:Cross-references: UNIPROT:Q9KNU3; UNIPARC:UPI000000C3360; GB:AE004330; GB:AE003652; NIT
A:Experimental source: serogroup O1; strain N16961; biotype El tor
C:Genetics:
A:Gene: VC2637
A:Map position: 1

Query Match 29.3%; Score 243.5; DB 2; Length 247;
Best Local Similarity 38.8%; Pred. No. 4.5e-15;
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 4;
Qy 5 KVGDAIPAV--EVEFEGEPGNKVNLAELFKGKGVLFVGPAFTPGCSKTHLPGFVEQAEAL 62
Db 9 KEGGTIPQVTPPTQGDAMVAVTSDLELFGKTVIVFSLPGAFTPTCSSHTLPRYNELAPV 68
Qy 63 LKAGVQVAVCLSVNDAFVTEGEMGRARAKGKVRLLADPTGAFGKETDLLDDSLVSIFG 122
Db 69 FKEHGVDSILCVSVNDTFVNAMAKDDQAD--NITFIPDNGCEFTDGMGLVYKNDLIG-FG 126
Qy 123 NRLLKRFSGNVQDGIYKALNVEPDGTG 149
Db 127 -KRSWRYSMVLVNGVVEKMFIEPNBPG 152

RESULT 14

AB0477
probable peroxiredoxin/glutaredoxin family protein YP03916 [imported] - *Yersinia pestis*
C:Species: *Yersinia pestis*
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB0477
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhal, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0477
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <KUR>
A:Cross-references: UNIPROT:Q8ZA95; UNIPARC:UPI000000DCAA0; GB:AL590842; PIDN:CAC93382.1;
C:Genetics:
A:Gene: YP03916

Query Match 27.2%; Score 225.5; DB 2; Length 243;
Best Local Similarity 36.6%; Pred. No. 2e-13;
Matches 53; Conservative 27; Mismatches 60; Indels 5; Gaps 4;
Qy 7 GDALPAV--EVEFEGEPGNKVNLAELFKGKGVLFVGPAFTPGCSKTHLPGFVEQAEAL 64
Db 7 GKVPQVTFHTROGDQWIDVTTDDLFSNKTIVFSLPGAFTPTCSSHTLPRYNELAPV 66
Qy 65 AKGVQVAVCLSVNDAFVTEGEMGRARAKGKVRLLADPTGAFGKETDLLDDSLVSIFGNR 124
Db 67 QHGVDSILCVSVNDTFVNAMAKSDQHA--NITFVPDNGCEFTKGMMLVERADLG-FGPR 124
Qy 125 RLKRFSGNVQDGIYKALNVEPDGTG 149
Db 125 SW-RYSMLVNGVVEKMFIEPNBPG 148

RESULT 15

164154
conserved hypothetical protein HI0572 - *Haemophilus influenzae* (strain Rd KW20)
C:Species: *Haemophilus influenzae*

C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: 164154
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirschner, E.F.; Kerlavage, A.
; Goetz, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Furman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A:Accession: 164154
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-241 <TTGR>
A:Cross-references: UNIPROT:P44758; UNIPARC:UPI0000139ABD; GB:U32739; GB:U42023; NID:915

Query Match 26.4%; Score 219.5; DB 2; Length 241;
Best Local Similarity 36.3%; Pred. No. 7.3e-13;
Matches 53; Conservative 27; Mismatches 59; Indels 7; Gaps 5;
Qy 7 GDALPAVEFEGEPGNK---VNLAELFKGKGVLFVGPAFTPGCSKTHLPGFVEQAEAL 63
Db 6 GKVPQV--TRTRQGDQWIDVTTSELFDNKTIVFSLPGAFTPTCSSHTLPRYNELAPV 64
Qy 64 KAKGVQVAVCLSVNDAFVTEGEMGRARAKGKVRLLADPTGAFGKETDLLDDSLVSIFGN 123
Db 65 KKGVDLIVSVNDTFVNAMAKDEKSE--NISFIPDNGCEFTDGMGLVYKNDLIG-FG- 121
Qy 124 RLKRFSGNVQDGIYKALNVEPDGTG 149
Db 122 KRSWRYSMVLVNGVVEKMFIEPNBPG 147

Search completed: February 21, 2006, 21:46:54
Job time : 40 secs

DR InterPro: IPR000866; Ahpc-TSA.
 DR InterPro: IPR012336; Thioredoxin-like.
 DR InterPro: IPR012335; Thioredoxin_fold.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KM Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;
 KM Peroxidase; Peroxisome; Polymorphism; Redox-active center;
 KW Transactin peptide.
 FT TRANSIT 1 ? Mitochondrion (potential).
 FT INIT MET 52 52 For isoform Cytoplasmic+peroxisomal.
 FT CHAIN 53 213 Peroxisome 5, isoform
 FT CHAIN 211 213 Cytoplasmic+peroxisomal.
 FT MOTIF 213 213 Peroxisome 5, isoform Mitochondrial.
 FT DISUPID 99 203 Microbody targeting signal (By
 FT VARIANT 68 68 Redox-activity).
 FT VARIANT 114 114 E -> G.
 FT VARIANT 130 130 L -> P.
 FT VARIANT 130 130 A -> V.
 SQ SEQUENCE 213 AA; 22179 MW; 9F0D03A4C87708A CRC64;
 Query Match 92.4%; Score 767; DB 1; Length 213;
 Best local Similarity 90.7%; Pred. No. 3,8e-60;
 Matches 147; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MAPIKVGDALPAVEVEEPEGPKVNLAELEFGKKGVLFGVPGAFTPGSKTHLPGFVEQA 60
 DB 52 MAPIKVGDITPSEVEEPEGPKVNLAELEFGKKGVLFGVPGAFTPGSKTHLPGFVEQA 111
 QY 61 EALKAGVQVAVCLSVNDAFTVGEWGRAHKAEGKRYLLADPTGAFGKETDILLDSLVSI 120
 DB 112 GALKAKGQVAVCLSVNDAFTVGEWGRAHKAEGKRYLLADPTGAFGKETDILLDSLVSI 171
 QY 121 FGNRLKRFSSMVQDGIYKALNVEPDGTGLTCSLAPNIIISQL 162
 DB 172 FGNRLKRFSSMVQDGIYKALNVEPDGTGLTCSLAPNIIISQL 213
 RESULT 7
 Q68G22 RAT PRELIMINARY; PRT; 213 AA.
 ID Q68G22: 068G22
 AC 068G22: 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Peroxisome 5.
 GN Name=Prdx5;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=101116;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RP TISSUE=Heart;
 RC NUCLEOTIDE SEQUENCE.
 RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schaller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Bismuth M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.N., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Spiller A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard L.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmov J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT *Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RA Director MGC Project;
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 DR EMBL: BC078773; AAH78773.1; -; mRNA.
 DR SMR: Q68G22; 53-213.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR InterPro: IPR012336; Thioredoxin-like.
 DR InterPro: IPR012335; Thioredoxin_fold.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KM Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.
 SQ SEQUENCE 213 AA; 22207 MW; 196A03BC61603825 CRC64;
 Query Match 91.9%; Score 763; DB 2; Length 213;
 Best local Similarity 90.1%; Pred. No. 8.7e-60;
 Matches 146; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MAPIKVGDALPAVEVEEPEGPKVNLAELEFGKKGVLFGVPGAFTPGSKTHLPGFVEQA 60
 DB 52 MAPIKVGDITPSEVEEPEGPKVNLAELEFGKKGVLFGVPGAFTPGSKTHLPGFVEQA 111
 QY 61 EALKAGVQVAVCLSVNDAFTVGEWGRAHKAEGKRYLLADPTGAFGKETDILLDSLVSI 120
 DB 112 GALKAKGQVAVCLSVNDAFTVGEWGRAHKAEGKRYLLADPTGAFGKETDILLDSLVSI 171
 QY 121 FGNRLKRFSSMVQDGIYKALNVEPDGTGLTCSLAPNIIISQL 162
 DB 172 FGNRLKRFSSMVQDGIYKALNVEPDGTGLTCSLAPNIIISQL 213
 RESULT 8
 Q6GLW8 PIG PRELIMINARY; PRT; 162 AA.
 ID Q6GLW8: 06GLW8
 AC 06GLW8: 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Peroxisome 5.
 GN Name=Prdx5;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OC NCBI_TaxID=9823;
 RX MEDLINE=10521424; DOI=10.1074/jbc.274.43.30451;
 RP TISSUE=Liver;
 RC NUCLEOTIDE SEQUENCE.
 RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schaller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Bismuth M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.N., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Spiller A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard L.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmov J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT *Generation and initial analysis of more than 15,000 full-length human

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strauberg R.L., Weingold E.A., Grouse L.H., Borge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bat N.A.,
 RA Hocking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stadler M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeck S.A., McEwen P.J., McKernan K.O., Malek J.A., Gutarra P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP PROTEIN SEQUENCE OF 50-61.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
 RL Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.,
 CC Subtilised (Aug-1998) to Swiss-Prot.
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with
 CC reducing equivalents provided through the thioredoxin system.
 CC -1- INVOLVED in intracellular redox signaling.
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Comment=2 isoforms, Mitochondrial (shown here) and
 CC Cytoplasmic+peroxisomal, are produced by alternative initiation;
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AF197951; AAF04855.1; -; mRNA.
 CC EMBL, AF124994; AAF27532.1; -; mRNA.
 CC EMBL, AF107333; AAG13450.1; -; mRNA.
 CC EMBL, AF208730; AAF21016.1; -; Genomic DNA.
 CC EMBL, AF208729; AAF21016.1; JOINED; Genomic DNA.
 CC EMBL, AK002383; BAB22058.1; -; mRNA.
 CC EMBL, AK003332; BAB22720.1; -; mRNA.
 CC EMBL, BC008174; AAH08174.1; -; mRNA.
 CC PIR, JCT239; JCT239.
 CC HSSP, P31004; 1HD2.
 CC SMR, P99029; 50-210.
 CC SWISS-2DPAGE, P99029; MOUSE.
 CC Ensemble, ENSMUSG0000024953; Mus musculus.
 CC MGI, MGI:1859821; Prdx5.
 CC GO, GO:0005739; Cytochrome; IDA.
 CC InterPro, IPR000866; Ahpc-TSA.
 CC InterPro, IPR012336; Thioredoxin-like.
 CC InterPro, IPR012335; Thioredoxin fold.
 CC Pfam, PF00578; Ahpc-TSA; 1.
 CC Alternative initiation; Antioxidant; Direct protein sequencing;
 CC Mitochondrion; Oxidoreductase; Peroxisome; Peroxisome;
 CC Redox-active center; Transit peptide.
 CC TRANSIT 1 Mitochondrion (Potential).
 CC INIT MET 49 49 For isoform Cytoplasmic+peroxisomal.
 CC CHAIN 50 210 Peroxiredoxin 5, isoform
 CC Cytoplasmic+peroxisomal.
 CC CHAIN ? 210 Peroxiredoxin 5, isoform Mitochondrial.

FT MOTIF 208 210 Microbody targeting signal (By
 FT DISULFID 96 200 similarity).
 FT CONFLICT 55 55 Redox-active (By similarity).
 FT CONFLICT 83 102 G->D (in Ref. 7).
 FT GULFVPGATPPGCKSKTHLP -> VPLGLESIGHLAVLR
 FT TA (in Ref. 4).
 SQ SEQUENCE 210 AA; 21897 MW; E944104CC468BD8 CRC64;
 Query Match 92.4%; Score 767; DB 1; Length 210;
 Best local similarity 91.4%; Pred. No. 3; Be-60;
 Matches 148; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MAPIKVDAIPAVEFEGEPGNKVNIAELFKKKGVLPVGAFTPCGSKTHLPVYQA 60
 DB 49 MAPIKVDAIPVSEFEGEPGNKVNIAELFKKKGVLPVGAFTPCGSKTHLPVYQA 108
 QY 61 EALAKGVQVAVACSVNDAFTGWSGAAHRAEGRVRLADPTGAFGETDILLDDISVSI 120
 DB 109 GALAKAGVAVACSVNDVFIEMGRAGRAHQAEGVRLADPTGAFGATDILLDDISVSI 168
 QY 121 FGNRLKRFMSVVDGIVKALNVBPDTGTLTCSLAFINISQL 162
 DB 169 FGNRLKRFMSVVDGIVKALNVBPDTGTLTCSLAFINISQL 210
 RESULT 6
 PDX5 RAT STANDARD PRT: 213 AA.
 ID PDX5 RAT STANDARD PRT: 213 AA.
 AC Q9R063;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Peroxiredoxin 5, mitochondrial precursor (BC 1.11.1.15) (Pxx-V)
 DE (Peroxisomal antioxidant enzyme) (PLP) (Thioredoxin reductase)
 DE (Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOB166).
 GN Name=Pdx5;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=99452929; PubMed=10521424; DOI=10.1074/jbc.274.43.30451;
 RA Knoops B., Clippe A., Bogard C., Areslane K., Watziez R., Hermans C.,
 RA Duconesille E., Falmagne P., Bernard A.,
 RT "Cloning and characterization of AOB166, a novel mammalian
 RT antioxidant enzyme of the peroxiredoxin family.";
 RL J. Biol. Chem. 274:30451-30458(1999).
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with
 CC reducing equivalents provided through the thioredoxin system.
 CC INVOLVED in intracellular redox signaling (By similarity).
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic
 CC (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, Mitochondrial (shown here) and
 CC Cytoplasmic+peroxisomal, are produced by alternative initiation;
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AF110732; AAF03751.1; -; mRNA.
 CC HSSP, P31004; 1HD2.
 CC SMR, Q9R063; 53-213.
 CC Ensemble, ENSRMUG0000021125; Rattus norvegicus.

SQ SEQUENCE 162 AA; 17324 MW; 8C6F98D1FA3B74D5 CRC64;
 Query Match 91.7%; Score 761; DB 2; Length 162;
 Best Local Similarity 90.7%; Pred. No. 9.7e-60;
 Matches 147; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 SQ SEQUENCE 219 AA; 23211 MW; 93C9B5D794A71581 CRC64;
 Query Match 90.0%; Score 747; DB 1; Length 219;
 Best Local Similarity 87.0%; Pred. No. 2.4e-58;
 Matches 141; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 Db 1 MAPIKGDPAIPAVEVEGEPEGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGEVQEA 60
 1 MAPIKGDPAIPSVVEVEGEPEGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGEVQEA 60
 Db 61 EALKAGVQVVAACLVNDVFTGEMGRANRKEGKRVLLADPTGAFGKETDILLDDSLVSI 120
 61 EALKAGVQVVAACLVNDVFTGEMGRANRKEGKRVLLADPTGAFGKETDILLDDSLVSI 120
 Db 121 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 162
 121 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 162
 Db 121 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 162
 121 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 162
 Db 178 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 219
 178 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 219
 RESULT 9
 PROX5 BOVIN STANDARD; PRT; 219 AA.
 ID PROX5_BOVIN STANDARD; PRT; 219 AA.
 AC O9BG11;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Peroxisredoxin 5, mitochondrial precursor (BC 1.11.1.15) (Per-V)
 DE (Thioredoxin reductase).
 GN Name=PROX5;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 ON [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Leyens G., Donay I., Knoops B.;
 RT Cloning of 4 new bovine peroxiredoxins, and screening of the complete
 RT peroxiredoxin family in different bovine tissues.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with
 CC reducing equivalents provided through the thioredoxin system.
 CC Involved in intracellular redox signaling (By similarity).
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic
 CC (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, Mitochondrial (shown here) and
 CC Cytoplasmic-peroxisomal, are produced by alternative initiation;
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AF305564; AAC53661.1; -; mRNA.
 CC HSSP; P30044; 1HD2.
 CC SMR; O9BG11; 59-219.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KM Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;
 KM Peroxisome; Peroxisome; Redox-active center; Transist peptide.
 FT TRANSIT 1 ? Mitochondrion (potential).
 FT INIT MET 58 58 For isoform Cytoplasmic+peroxisomal.
 FT CHAIN 59 219 Peroxisredoxin 5, isoform
 FT Cytoplasmic+peroxisomal.

FT CHAIN ? 219 Peroxisredoxin 5, isoform Mitochondrial.
 FT MOTIF 217 219 Microbody targeting signal (By
 FT DISULFID 105 209 similarity). (By similarity).
 FT SEQUENCE 219 AA; 23211 MW; 93C9B5D794A71581 CRC64;
 SQ SEQUENCE 219 AA; 23211 MW; 93C9B5D794A71581 CRC64;
 Query Match 90.0%; Score 747; DB 1; Length 219;
 Best Local Similarity 87.0%; Pred. No. 2.4e-58;
 Matches 141; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 Db 1 MAPIKGDPAIPAVEVEGEPEGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGEVQEA 60
 1 MAPIKGDPAIPSVVEVEGEPEGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGEVQEA 60
 Db 58 MAPIKGDPAIPSVVEVEGEPEGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGEVQEA 117
 58 MAPIKGDPAIPSVVEVEGEPEGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGEVQEA 117
 Db 61 EALKAGVQVVAACLVNDVFTGEMGRANRKEGKRVLLADPTGAFGKETDILLDDSLVSI 120
 61 EALKAGVQVVAACLVNDVFTGEMGRANRKEGKRVLLADPTGAFGKETDILLDDSLVSI 120
 Db 118 DALKKAGVQVVAACLVNDVFTGEMGRANRKEGKRVLLADPTGAFGKETDILLDDSLVSI 177
 118 DALKKAGVQVVAACLVNDVFTGEMGRANRKEGKRVLLADPTGAFGKETDILLDDSLVSI 177
 Db 121 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 162
 121 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 162
 Db 178 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 219
 178 FGNRLKRFPSMVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 219
 RESULT 10
 O9D6X2 MOUSE
 ID O9D6X2_MOUSE PRELIMINARY; PRT; 211 AA.
 AC O9D6X2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched
 DE library, clone:2310046N07 product:peroxiredoxin 6, full insert
 DE sequence.
 GN Name=Prox5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 ON [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kabukawa T., Saito R.,
 RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Niki K., Pesole G., Quackenbush J.,
 RA Schriml L. M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Oikawa T., Furuno M., Aono H., Balarelli R., Barsh G.,
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M. F.,
 RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamuya M., Lee N. H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J. J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K. F.,
 RA Suzuki H., Toyokawa K., Wang K. H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT *Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;

RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team.
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs." ;
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y. ;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes." ;
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsumi T., Taahiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y. ;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer." ;
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Koda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y. ;
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 DR EMBL; AK009859; BAB26548.1; -; mRNA.
 DR HSSP; P30044; 1HD2.
 DR SMR; Q9D6X2; 54-211.
 DR Ensembl; ENSMUSG0000024953; Mus musculus.
 DR MGI; MGI:1859821; Prdx5.
 DR GO; GO:0005739; C:mitochondrion; IDA.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR InterPro; IPR012336; Thiorodoxin-like.
 DR InterPro; IPR012335; Thiorodoxin-fold.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.
 SQ SEQUENCE 211 AA; 22500 MW; 676B009BC6E10098 CRC64;
 QY
 Query Match 87.6%; Score 727; DB 2; Length 211;
 Best Local Similarity 89.2%; Pred. No. 1.4e-56;
 Matches 111; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
 DB 54 KVGDAIIVSEVGESEKKNVLAELFKGKGVLFVGAFATPCGYKTHLPGVEQAKALK 113
 QY 5 KVGDAIIVSEVGESEKKNVLAELFKGKGVLFVGAFATPCGYKTHLPGVEQAKALK 64
 DB 65 AKGVQVACIIVNDATVTEGEMGAKHAKAEGRVRLAAPTGAFGENTLLDDSVITINR 124
 QY 114 AKGAQVAVACIIVNDATVTEGEMGAKHAKAEGRVRLAAPTGAFGATLLDDSVLISFGAK 173
 DB 125 RLKRFSSVVDGIVKLVNVEPDTGLTCSLAPNIIISQL 162
 QY 174 RLKRFSSVVDGIVKLVNVEPDTGLTCSLAPNIIISQL 211

RESULT 11
 Q6GPY3_XENLA PRELIMINARY; PRT; 189 AA.
 ID Q6GPY3;
 AC Q6GPY3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE MGCS2521 protein.
 GN Name=MGCS2521;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.T., Skalska J., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A. ;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strusberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P. ;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative." ;
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX TISSUE=Spleen;
 RA Klein S., Gerhard D.S. ;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
 DR EMBL; BC072972; AAH72972.1; -; mRNA.
 DR SMR; Q6GPY3; 30-189.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR InterPro; IPR012336; Thiorodoxin-like.
 DR InterPro; IPR012335; Thiorodoxin-fold.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.
 SQ SEQUENCE 189 AA; 20066 MW; 5EA78C7EBD24D808 CRC64;
 QY
 Query Match 70.3%; Score 583.5; DB 2; Length 189;
 Best Local Similarity 70.0%; Pred. No. 7.3e-44;
 Matches 112; Conservative 17; Mismatches 30; Indels 1; Gaps 1;
 DB 4 IKVGAIIVSEVGESEKKNVLAELFKGKGVLFVGAFATPCGYKTHLPGVEQAKALK 63
 QY 30 IKVGAIIVSEVGESEKKNVLAELFKGKGVLFVGAFATPCGYKTHLPGVEQAKALK 89

Qy 64 KAKGVVAVCLSVNDVAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIIFG 122
 Db 90 KSRGAIVAVCLSVNDVAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIIFG 149
 Qy 123 NRRLKRFPSMVVODGIYKALNVEPDGTGLTCSLAPNIISOL 162
 Db 150 NORCRFSFMSVVEDGKIKALNVEPDGTGLTCSLAPNIISOL 189

RESULT 12

Q502C8 BRABE PRELIMINARY; PRT; 162 AA.
 ID Q502C8 BRABE PRELIMINARY; PRT; 162 AA.
 AC Q502C8
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein zgc:112318.
 GN ORFNames=zgc:112318;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 CX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.2426038999;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Alechuth S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Matusin K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalski U., Smallos D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RC NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2O) + ROH.
 DR EMBL; BC095755; AAH95755.1; -; mRNA.
 DR Ensemble; ENSDARG00000020317; Danio rerio.
 DR ZFIN; ZDB-GENE-050522-159; zgc:112318.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR InterPro; IPR012335; Thioresoxin-like.
 DR InterPro; IPR012335; Thioresoxin-like.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 DR Antioxidant; Hypothetical protein; Oxidoreductase; Peroxidase;
 KW Redox-active center.
 SQ SEQUENCE 162 AA; 17109 MW; 5C7C1CE753E0B41 CRC64;

Query Match 64.6%; Score 536.5; DB 2; Length 162;
 Best Local Similarity 60.9%; Pred. No. 9.4e-40;
 Matches 98; Conservative 33; Mismatches 29; Indels 1; Gaps 1;

Qy 3 PIRKGDALPAVEVEGEBGNKVNLAELFKGKKGVLFVPGAFPTGCSKTHLPGEVQAEA 62
 Db 2 PIRKGDALPAVEVEGEBGNKVNLAELFKGKKGVLFVPGAFPTGCSKTHLPGEVQAEA 61
 Qy 63 LKAGVAVVAVCLSVNDVAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIIF 121

Db 62 LKAGVAVVAVCLSVNDVAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIIF 121
 Qy 122 GNRLKRFPSMVVODGIYKALNVEPDGTGLTCSLAPNIISOL 162
 Db 122 GNRLKRFPSMVVODGIYKALNVEPDGTGLTCSLAPNIISOL 162

RESULT 13

Q8T5Q7 BRABE PRELIMINARY; PRT; 188 AA.
 ID Q8T5Q7 BRABE PRELIMINARY; PRT; 188 AA.
 AC Q8T5Q7
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Peroxisome oxidin V protein.
 GN Name=AmpHixV;
 OS Branchiostoma belcheri tsingtauense.
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 CC Branchiostoma.
 CX NCBI_TaxID=155462;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Zhang S., Liu Z., Yuan J., Liu M., Wei J., Xu A.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2O) + ROH.
 DR EMBL; AF498232; AAM18076.1; -; mRNA.
 DR HSSP; P30044; IHD2.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR InterPro; IPR012335; Thioresoxin-like.
 DR InterPro; IPR012335; Thioresoxin-like.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.
 SQ SEQUENCE 188 AA; 19802 MW; 3FCB6C23AA0B2726 CRC64;

Query Match 63.1%; Score 524; DB 2; Length 188;
 Best Local Similarity 65.4%; Pred. No. 1.4e-38;
 Matches 102; Conservative 18; Mismatches 34; Indels 2; Gaps 1;

Qy 3 PIRKGDALPAVEVEGEBGNKVNLAELFKGKKGVLFVPGAFPTGCSKTHLPGEVQAEA 62
 Db 33 PIRKGDALPAVEVEGEBGNKVNLAELFKGKKGVLFVPGAFPTGCSKTHLPGEVQAEA 92
 Qy 63 LKAGVAVVAVCLSVNDVAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIIF 122
 Db 93 LKAGVAVVAVCLSVNDVAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIIF 150
 Qy 123 NRRLKRFPSMVVODGIYKALNVEPDGTGLTCSLAPNIISOL 162
 Db 151 NRRLKRFPSMVVODGIYKALNVEPDGTGLTCSLAPNIISOL 186

RESULT 14

Q5UG08 AEDAE PRELIMINARY; PRT; 157 AA.
 ID Q5UG08 AEDAE PRELIMINARY; PRT; 157 AA.
 AC Q5UG08
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Peroxisome oxidin-like protein.
 OS Aedes aegypti (Yellow fever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 CC Culicinae; Culicini; Aedes; Stegomyia.
 CX NCBI_TaxID=7159;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Salivary gland;
 RA Chandra P.K., Wikel S.K.,
 RT "Complementing the salivome of the adult female Aedes aegypti
 RT mosquito.";

Qy 3 PIRKGDALPAVEVEGEBGNKVNLAELFKGKKGVLFVPGAFPTGCSKTHLPGEVQAEA 62
 Db 2 PIRKGDALPAVEVEGEBGNKVNLAELFKGKKGVLFVPGAFPTGCSKTHLPGEVQAEA 61
 Qy 63 LKAGVAVVAVCLSVNDVAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIIF 121

RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Conjugation of reduced glutathione to a wide number of
CC exogenous and endogenous hydrophobic electrophiles (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
CC -!- SUBUNIT: Homodimer (By similarity).
DR EMBL; AY738253; AAV4853.1; -; mRNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR InterPro; IPR000666; Ahpc-TSA.
DR InterPro; IPR012336; Thiooxidin-like.
DR InterPro; IPR012335; Thiooxidin fold.
DR Pfam; PF00578; Ahpc-TSA; 1.
KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.
SQ SEQUENCE 157 AA; 16644 MW; 02E974DB7723DBE6 CRC64;

Query Match 59.6%; Score 494.5; DB 2; Length 157;
Best Local Similarity 58.2%; Pred. No. 5e-36;
Matches 92; Conservative 26; Mismatches 37; Indels 3; Gaps 1;

QY 1 MAPIKVGDALPAVEVEGEGRNKVNLAELFKGKGVLPFGAFTPGCSKTHLPGFVEQA 60
DB 1 MWQIKEGDKIPSIDLFEDSPANKVMADLCAGKVVLPFAVPGAFTPGCSKTHLPGVDR 60
QY 61 EALKAKGVVAVACLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDLSVSI 120
DB 61 DAIKSSGVEIYCVSNDPFWMSAWGKOHNTGKVRMLADPAALFTKQLELAD--LPP 117
QY 121 FGNRLKRFSMVVDGIVKALNVEPDGTGLTCSLAPNI 158
DB 118 LGGLRSKRYSMVLBDGVKSLNVEPDGTGLSCSLADKI 155

RESULT 15
Q7PUM1_ANOGA
ID Q7PUM1 ANOGA PRELIMINARY; PRT; 246 AA.
AC Q7PUM1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000020393 (Fragment).
GN ORFNames=ENSANG00000017904;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nemotoceera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OK NCBI_TaxId=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST.
RA Anopheles Genome Sequencing Consortium.
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.
DR EMBL; AAB01008987; EAA01313.2; -; Genomic_DNA.
DR HSSP; P30044; 1HD2.
DR GO; GO:0016209; F:antioxidant activity; IEA.
DR InterPro; IPR000866; Ahpc-TSA.
DR InterPro; IPR012336; Thiooxidin-like.
DR InterPro; IPR012335; Thiooxidin fold.
DR Pfam; PF00578; Ahpc-TSA; 1.
KW Antioxidant.
FT NON_TER 1
SQ SEQUENCE 246 AA; 26218 MW; 4CACCB3F50C8E2A3 CRC64;

Query Match 58.6%; Score 486.5; DB 2; Length 246;
Best Local Similarity 58.9%; Pred. No. 4.2e-35;
Matches 93; Conservative 22; Mismatches 40; Indels 3; Gaps 1;

QY 1 MAPIKVGDALPAVEVEGEGRNKVNLAELFKGKGVLPFGAFTPGCSKTHLPGFVEQA 60
DB 1 MWQIKEGDKIPSIDLFEDSPANKVMADLCAGKVVLPFAVPGAFTPGCSKTHLPGVDR 60

DB 90 MWQIKEGDKIPSIDLFEDSPANKVMADLCAGKVVLPFAVPGAFTPGCSKTHLPGFVEKA 149
QY 61 EALKAKGVVAVACLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDLSVSI 120
DB 150 GDLKSSGATEIYCVSNDPFWMSAWGKOHNTGKVRMLADPAALFTKQLELAD--LPP 206
QY 121 FGNRLKRFSMVVDGIVKALNVEPDGTGLTCSLAPNI 158
DB 207 LGGLRSKRYSMVLBDGVKSLNVEPDGTGLSCSLADKI 244

Search completed: February 21, 2006, 21:46:11
Job time : 234 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:57:41 ; Search time 168 Seconds
(without alignments)
402.907 Million cell updates/sec

Title: US-10-686-157-2
Perfect score: 830
Sequence: 1 MAPKVGDAIPAVEFESEGP.....VEPDGTGLTCSLAPNISQL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	830	100.0	162	US-10-408-765A-2152	Sequence 2152, Ap
2	830	100.0	162	US-10-686-157-2	Sequence 2, Appli
3	830	100.0	205	US-10-276-774-1773	Sequence 1773, Ap
4	830	100.0	214	US-10-394-116-1	Sequence 1, Appli
5	830	100.0	214	US-10-408-765A-770	Sequence 770, App
6	830	100.0	214	US-10-974-148-20	Sequence 20, Appl
7	830	100.0	214	US-10-686-157-21	Sequence 21, Appl
8	825	99.4	161	US-10-408-765A-2397	Sequence 2397, Ap
9	777	93.6	226	US-10-264-049-3514	Sequence 3514, Ap
10	767	92.4	162	US-10-686-157-6	Sequence 6, Appli
11	752	90.6	162	US-10-686-157-4	Sequence 4, Appli
12	747	90.0	219	US-10-732-923-21551	Sequence 21551, A
13	725	87.3	217	US-10-424-599-246448	Sequence 246448, A
14	667	80.4	150	US-10-263-828-97	Sequence 97, Appl
15	573	69.0	169	US-10-491-183-16	Sequence 16, Appl
16	569	68.6	351	US-10-450-763-51040	Sequence 51040, A
17	524	63.1	188	US-10-732-923-21448	Sequence 21448, A
18	498	60.0	137	US-10-972-024-470	Sequence 470, App
19	481	58.0	190	US-10-732-923-21547	Sequence 21547, A
20	479	57.7	157	US-11-097-143-16080	Sequence 16080, A
21	476.5	57.4	153	US-10-732-923-21451	Sequence 21451, A
22	475.5	57.3	175	US-10-732-923-21450	Sequence 21450, A
23	469.5	56.6	285	US-10-450-763-39760	Sequence 39760, A
24	400.5	48.3	185	US-10-732-923-21545	Sequence 21545, A
25	349	42.0	125	US-10-972-024-178	Sequence 178, App
26	346	41.7	130	US-10-264-049-3474	Sequence 3474, Ap
27	332	40.0	183	US-10-767-701-51758	Sequence 51758, A

28	317	38.2	161	5	US-10-732-923-21458	Sequence 21458, A
29	317	38.2	191	5	US-10-732-923-21466	Sequence 21466, A
30	313.5	37.8	202	5	US-10-732-923-21447	Sequence 21447, A
31	312.5	37.7	160	5	US-10-732-923-21456	Sequence 21456, A
32	310.5	37.4	160	5	US-10-732-923-21462	Sequence 21462, A
33	310.5	37.4	163	5	US-10-732-923-21518	Sequence 21518, A
34	310.5	37.3	162	4	US-10-310-154-687	Sequence 687, App
35	310	37.3	162	5	US-10-732-923-21516	Sequence 21516, A
36	310	37.3	162	5	US-10-732-923-21517	Sequence 21517, A
37	310	37.3	215	4	US-10-424-599-244213	Sequence 244213, A
38	310	37.3	248	4	US-10-425-114-51447	Sequence 51447, A
39	310	37.3	249	5	US-10-732-923-21493	Sequence 21493, A
40	309.5	37.3	159	5	US-10-732-923-21527	Sequence 21527, A
41	308.5	37.2	196	5	US-10-732-923-21534	Sequence 21534, A
42	308	37.1	157	5	US-10-732-923-21463	Sequence 21463, A
43	306	36.9	162	4	US-10-424-599-257249	Sequence 257249, A
44	305	36.7	158	5	US-10-732-923-21460	Sequence 21460, A
45	303	36.5	161	5	US-10-732-923-21453	Sequence 21453, A

ALIGNMENTS

```

RESULT 1
US-10-408-765A-2152
; Sequence 2152, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2152
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2152

Query Match      100.0%; Score 830; DB 4; Length 162;
Best local similarity 100.0%; Pred. No. 4.8e-85;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAPKVGDAIPAVEFESEGNKYNLAELFGKKGVLFVGAFPTGCGSKTHLPQFYQA 60
        |||
DB      1 MAPKVGDAIPAVEFESEGNKYNLAELFGKKGVLFVGAFPTGCGSKTHLPQFYQA 60
        |||

QY      61 EALAKGVQVAVACSVNDAFTTGWGRRAHKBGVRIADPTGAFGKETDILLDSYVI 120
        |||
DB      61 EALAKGVQVAVACSVNDAFTTGWGRRAHKBGVRIADPTGAFGKETDILLDSYVI 120
        |||

QY      121 FGNRLKRFMSWVVDGIVKALNVDPDGTGLTCSLAPNISQL 162
        |||
DB      121 FGNRLKRFMSWVVDGIVKALNVDPDGTGLTCSLAPNISQL 162
        |||

RESULT 2
US-10-686-157-2
; Sequence 2, Application US/10686157
; Publication No. US20050142126A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
; APPLICANT: UNIVERSITE DE MONS-HAINAUT
; TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding

```

```

1  TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment
2  TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related
3  TITLE OF INVENTION: disorders
4  TITLE OF INVENTION: disorders
5  FILE REFERENCE: DECL350.001CPI
6  CURRENT APPLICATION NUMBER: US/10/686,157
7  CURRENT FILING DATE: 2003-10-15
8  PRIOR APPLICATION NUMBER: US 6,759,194
9  PRIOR FILING DATE: 2000-08-15
10 PRIOR APPLICATION NUMBER: PCT/BE98/00124
11 PRIOR FILING DATE: 1998-08-20
12 PRIOR APPLICATION NUMBER: BE 1011331
13 PRIOR FILING DATE: 1997-08-20
14 NUMBER OF SEQ ID NOS: 21
15 SOFTWARE: PatentIn version 3.3
16 SEQ ID NO 2
17 LENGTH: 162
18 TYPE: PRT
19 ORGANISM: Homo sapiens
20 US-10-686-157-2

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Query Match	100.0%;	Score 830;	DB 5;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 4.8e-85;		
Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MAPKVGDAIPAVEVEGEGGNKVNIAELFFKKKKVLGVGPAPFGSKTHLPGFPEQA	60
Db	1	MAPLKGDALPAVEVEGEGGNKVNIAELFFKKKKVLGVGPAPFGSKTHLPGFPEQA	60
Qy	61	EALKAKGVQVACLSVNDAFVTGGEWRARHAKGKRLADPTGAFGKSTDLTLDLSVSI	120
Db	61	EALKAKGVQVACLSVNDAFVTGGEWRARHAKGKRLADPTGAFGKSTDLTLDLSVSI	120
Qy	121	FGNRRLEKRFSMVQDGIIVKALANPEPGSTGLTCSLAPNIISQI	162
Db	121	FGNRRLEKRFSMVQDGIIVKALANPEPGSTGLTCSLAPNIISQI	162

```

RESULT 3
US-10-276-774-1773
; Sequence 1773, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: NO. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276, 774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560, 875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496, 914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1773
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1773

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Query Match	100.0%	Score 830	DB 4	Length 205
Best Local Similarity	100.0%	Pred. No. 6.6e-85		
Matches 163	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MAPIKVGAIPAVEVFEGEGPGKNVLAELFKKKGVLFVGPAGAPPGSKTHLPGFVEOA	60	
Db	44	MAPIVGGAIPAVEVFEGEGPGKNVLAELFKKKGVLFVGPAGAPPGSKTHLPGFVEOA	103	
Qy	61	EALKAGVQVVACTSVNDAPVTEGEGRAHKEGKRVLLADPGAGKETDLLDDSLYSI	120	
Db	104	EALKAGVQVVACTSVNDAPVTEGEGRAHKEGKRVLLADPGAGKETDLLDDSLYSI	163	
Qy	121	FGNRLKRFPMVVDGIYKALNVEPDGTLCTSLAPNTISQL	162	

Db 164 FGNRLKRFSMVQDGIKALNVEPDGTGLTCSLAENIISQL 205

```

RESULT 4
US-10-394-136-1
: Sequence 1, Application US/10394136
: Publication No. US20030175787A1
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Yue, Henry
: APPLICANT: Lal, Preeti
: APPLICANT: Kaser, Matthew R.
: TITLE OF INVENTION: VESICLE MEMBRANE PROTEINS
: FILE REFERENCE: PC-0029 CIP
: CURRENT APPLICATION NUMBER: US/10/394,136
: CURRENT FILING DATE: 2003-03-19
: PRIOR APPLICATION NUMBER: US/09/718,996
: PRIOR FILING DATE: 2000-11-22
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PERL Program
: SEQ ID NO 1
: LENGTH: 214
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. US20030175787A1 743725
US-10-394-136-1

```

Query Match	100.0%;	Score 830;	DB 4;	Length 214;
Best Local Similarity	100.0%;	Pred. No. 7e-85;		
Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	MAPIKYGDAIPAVEVEBEGPKNVLAEIFGKGGVLGVGATLPGCSKTHLGFVEQA	60
Db	MAPIKYGDAIPAVEVEBEGPKNVLAEIFGKGGVLGVGATLPGCSKTHLGFVEQA	112
Qy	MAPIKYGDAIPAVEVEBEGPKNVLAEIFGKGGVLGVGATLPGCSKTHLGFVEQA	120
Db	MAPIKYGDAIPAVEVEBEGPKNVLAEIFGKGGVLGVGATLPGCSKTHLGFVEQA	172
Qy	EALKKAGVQVACLSTNDAFVTGPEGRHAKBEGKRYLLADPTGAFGETLLLDLSVSI	214
Db	EALKKAGVQVACLSTNDAFVTGPEGRHAKBEGKRYLLADPTGAFGETLLLDLSVSI	266
Qy	EALKKAGVQVACLSTNDAFVTGPEGRHAKBEGKRYLLADPTGAFGETLLLDLSVSI	274
Db	EALKKAGVQVACLSTNDAFVTGPEGRHAKBEGKRYLLADPTGAFGETLLLDLSVSI	326
Qy	FGNRRLLKRFPSMVVODGIVKALNVEPDGTGLTCSLAPNIIISQL	362
Db	FGNRRLLKRFPSMVVODGIVKALNVEPDGTGLTCSLAPNIIISQL	414
Qy	FGNRRLLKRFPSMVVODGIVKALNVEPDGTGLTCSLAPNIIISQL	422
Db	FGNRRLLKRFPSMVVODGIVKALNVEPDGTGLTCSLAPNIIISQL	474

```

RESULT 5
US-10-408-765A-770
; Sequence 770, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Colin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-770

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Query Match 100.0%; Score 830; DB 4; Length 214;

Best Local Similarity 100.0%; Pred. No. 7e-85;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPGEVQAE 60
DB 53 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPGEVQAE 112
QY 61 EALAKGVQVAACTSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDDSLVSI 120
DB 113 EALAKGVQVAACTSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDDSLVSI 172
QY 121 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISQL 162
DB 173 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISQL 214

RESULT 6
US-10-974-148-20

; Sequence 20, Application US/10974148
; Publication No. US20050123962A1

GENERAL INFORMATION:

; APPLICANT: Gan, Li

; APPLICANT: Gonzalez-Zulueta, Mirella

; APPLICANT: Ye, Shiming

; APPLICANT: Uferer, Roman

; TITLE OF INVENTION: Regulated Nucleic Acids in Pathogenesis of Alzheimer's Disease

; FILE REFERENCE: AGT-048

; CURRENT APPLICATION NUMBER: US/10/974,148

; CURRENT FILING DATE: 2004-10-26

; PRIOR APPLICATION NUMBER: 60/515,536

; PRIOR FILING DATE: 2003-10-28

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: Patent version 3.2

; SEQ ID NO 20

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-974-148-20

Query Match 100.0%; Score 830; DB 5; Length 214;

Best Local Similarity 100.0%; Pred. No. 7e-85;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPGEVQAE 60
DB 53 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPGEVQAE 112
QY 61 EALAKGVQVAACTSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDDSLVSI 120
DB 113 EALAKGVQVAACTSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDDSLVSI 172
QY 121 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISQL 162
DB 173 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISQL 214

RESULT 7
US-10-686-157-21

; Sequence 21, Application US/10686157

; Publication No. US20050142126A1

GENERAL INFORMATION:

; APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN

; APPLICANT: UNIVERSITE DE MONS-HAINAUT

; TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding

; TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment

; TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related

; FILE REFERENCE: DECLE30.001CPI

; CURRENT APPLICATION NUMBER: US/10/686,157

; CURRENT FILING DATE: 2003-10-15

; PRIOR APPLICATION NUMBER: US 6,759,194

; PRIOR FILING DATE: 2000-08-15

; PRIOR APPLICATION NUMBER: PCT/BE98/00124

; PRIOR FILING DATE: 1998-08-20

; PRIOR APPLICATION NUMBER: BE 1011331

; PRIOR FILING DATE: 1997-08-20

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patent version 3.3

; SEQ ID NO 21

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-686-157-21

Query Match 100.0%; Score 830; DB 5; Length 214;

Best Local Similarity 100.0%; Pred. No. 7e-85;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPGEVQAE 60
DB 53 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPGEVQAE 112
QY 61 EALAKGVQVAACTSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDDSLVSI 120
DB 113 EALAKGVQVAACTSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDDSLVSI 172
QY 121 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISQL 162
DB 173 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISQL 214

RESULT 8
US-10-408-765A-2397

; Sequence 2397, Application US/10408765A

; Publication No. US20040101874A1

GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Eoin D.

; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.

; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408,765A

; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2397

; LENGTH: 161

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-2397

Query Match 99.4%; Score 825; DB 4; Length 161;

Best Local Similarity 100.0%; Pred. No. 1.7e-84;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APIKVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPGEVQAE 61
DB 1 APIKVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPGEVQAE 60
QY 62 ALKAKGVQVAACTSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDDSLVSI 121
DB 61 ALKAKGVQVAACTSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDDSLVSI 120
QY 122 GNRRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISQL 162
DB 121 GNRRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISQL 161

RESULT 9
US-10-264-049-3514


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; Sequence 3514, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3514
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (79)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (90)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (110)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (190)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (225)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; US-10-264-049-3514

Query Match          93.6%; Score 777; DB 4; Length 226;
Best Local Similarity 95.1%; Pred. No. 7,1e-79;
Matches 154; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAPIVGDAIPAVEVEBEPGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGFVEQA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 52 MAPIVGDAIPAVEVEBEPGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGFVEQA 111
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 EALKKAGVAVACISVNDAPFTTGEMGRARAKAGKRVRLADPTGARGKETDILLDSIVSI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 112 EALKKAGVAVACISVNDAPFTTGEMGRARAKAGKRVRLADPTGARGKETDILLDSIVSI 171
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FGNRLKRFMSWVVDGIVKALNVEPDGTGLTCSLAPNIISOL 162
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 172 FGNRLKRFMSWVVDGIVKALNVEPDGTGLTCSLAPNIISOL 213
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-10-686-157-6
; Sequence 6, Application US/10686157
; Publication No. US20050142126A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
; APPLICANT: UNIVERSITE DE MONS-HAINAUT
; TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding
```

```
; TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment
; TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related
; FILE REFERENCE: DECLE30.001CP1
; CURRENT APPLICATION NUMBER: US/10/686,157
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 6,759,194
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: PCT/BE98/00124
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: BE 1011331
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-686-157-6

Query Match          92.4%; Score 767; DB 5; Length 162;
Best Local Similarity 91.4%; Pred. No. 6,1e-78;
Matches 148; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAPIVGDAIPAVEVEBEPGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGFVEQA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MAPIVGDAIPAVEVEBEPGNKVNLAELFKGKGVLFVGPAGFTPGCSKTHLPGFVEQA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 EALKKAGVAVACISVNDAPFTTGEMGRARAKAGKRVRLADPTGARGKETDILLDSIVSI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EALKKAGVAVACISVNDAPFTTGEMGRARAKAGKRVRLADPTGARGKETDILLDSIVSI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FGNRLKRFMSWVVDGIVKALNVEPDGTGLTCSLAPNIISOL 162
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 FGNRLKRFMSWVVDGIVKALNVEPDGTGLTCSLAPNIISOL 162
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-10-686-157-4
; Sequence 4, Application US/10686157
; Publication No. US20050142126A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
; APPLICANT: UNIVERSITE DE MONS-HAINAUT
; TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding
; TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment
; TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related
; FILE REFERENCE: DECLE30.001CP1
; CURRENT APPLICATION NUMBER: US/10/686,157
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 6,759,194
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: PCT/BE98/00124
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: BE 1011331
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)..(17)
; OTHER INFORMATION: X = E or G
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (63)..(63)
; OTHER INFORMATION: X = L or P
; FEATURE:
; NAME/KEY: MISC_FEATURE
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LOCATION: (79)..(79)
OTHER INFORMATION: X = L or P
US-10-686-157-4

Query Match 90.6%; Score 752; DB 5; Length 162;
Best Local Similarity 88.9%; Pred. No. 3e-76;
Matches 144; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEFEGEPGNKNVLAELFKGKGVLFPGVGAFTPGCKSTHLLPGFVEQA 60
DB 1 MAPIKVGDALPAVEFEGEPGNKNVLAELFKGKGVLFPGVGAFTPGCKSTHLLPGFVEQA 60
QY 61 EALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
DB 61 GAXAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
QY 121 FGNRLKRFPSNVODGIVKALNVEPDGTGLTCSLAPNIIISQL 162
DB 121 FGNRLKRFPSNVODGIVKALNVEPDGTGLTCSLAPNIIISQL 162

RESULT 12

US-10-732-923-21551
Sequence 21551, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 21551
LENGTH: 219
TYPE: PRT
ORGANISM: Bos taurus
US-10-732-923-21551

Query Match 90.0%; Score 747; DB 5; Length 219;
Best Local Similarity 87.0%; Pred. No. 1.6e-75;
Matches 141; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEFEGEPGNKNVLAELFKGKGVLFPGVGAFTPGCKSTHLLPGFVEQA 60
DB 58 MAPIKVGDALPAVEFEGEPGNKNVLAELFKGKGVLFPGVGAFTPGCKSTHLLPGFVEQA 117
QY 61 EALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
DB 118 DALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 177
QY 121 FGNRLKRFPSNVODGIVKALNVEPDGTGLTCSLAPNIIISQL 162
DB 178 FGNRLKRFPSNVODGIVKALNVEPDGTGLTCSLAPNIIISQL 219

RESULT 13

US-10-424-599-246448
Sequence 246448, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 246448

LENGTH: 217
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(217)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_64574C.1 pep
US-10-424-599-246448

Query Match 87.3%; Score 725; DB 4; Length 217;
Best Local Similarity 86.4%; Pred. No. 4.9e-73;
Matches 140; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEFEGEPGNKNVLAELFKGKGVLFPGVGAFTPGCKSTHLLPGFVEQA 60
DB 53 MAPIKVGDALPAVEFEGEPGNKNVLAELFKGKGVLFPGVGAFTPGCKSTHLLPGFVEQA 112
QY 61 EALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
DB 113 GALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172
QY 121 FGNRLKRFPSNVODGIVKALNVEPDGTGLTCSLAPNIIISQL 162
DB 173 FGNRLKRFPSNVODGIVKALNVEPDGTGLTCSLAPNIIISQL 214

RESULT 14

US-10-263-828-97
Sequence 97, Application US/10263828
Publication No. US20030138905A1
GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: mammary gland and methods for their use.
FILE REFERENCE: 11000.10440icon
CURRENT APPLICATION NUMBER: US/10/263,828
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97
LENGTH: 150
TYPE: PRT
ORGANISM: Bovine
US-10-263-828-97

Query Match 80.4%; Score 667; DB 4; Length 150;
Best Local Similarity 87.0%; Pred. No. 1e-66;
Matches 127; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEFEGEPGNKNVLAELFKGKGVLFPGVGAFTPGCKSTHLLPGFVEQA 60
DB 5 MAPIKVGDALPAVEFEGEPGNKNVLAELFKGKGVLFPGVGAFTPGCKSTHLLPGFVEQA 64
QY 61 EALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
DB 65 DALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 124
QY 121 FGNRLKRFPSNVODGIVKALNVEPD 146
DB 125 FGNRLKRFPSNVODGIVKALNVEPD 150

RESULT 15

US-10-491-183-16
Sequence 16, Application US/10491183
Publication No. US20050191627A1
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION;YANG, Junming

```

; APPLICANT: LU, Dzung, Alina M.; YUE, Henry
; APPLICANT: ELIOT, Vicki S.; WARREN, Bridget A.
; APPLICANT: DUGGAN, Brendan M.; FORSYTHE, Ian J.
; APPLICANT: LEE, Ernestine A.; HAPALIA, April J. A.
; APPLICANT: RAMKUMAR, Jayalakmi; CHAMLA, Narinder K.
; APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.
; APPLICANT: GORVAD, Ann E.; TRAN, Uyen K.
; APPLICANT: LI, Joana X.; YAO, Monique G.
; APPLICANT: ISON, Craig H.; GRIFFIN, Jennifer A.
; APPLICANT: LEE, Soo Yeun; CHANG, Hei-Ru
; APPLICANT: EMERLING, Brooke M.; TANG, Y. Tom
; APPLICANT: LAL, Preeti G.; KABLE, Amy E.
; APPLICANT: MARQUIS, Joseph P.; JIANG, Xin
; APPLICANT: JACKSON, Alan A.; ZEBARJADIAN, Yeganeh
; APPLICANT: SWARNAKAR, Anita; WILSON, Amy D.
; APPLICANT: JIN, Pei; RICHARDSON, Thomas W.
; APPLICANT: BHATIA, Umesh; BURRILL, John D.
; APPLICANT: LEE, Sally; BLAKE, Julie J.
; APPLICANT: HO, Anne; ZHENG, Wenjin
; APPLICANT: GAO, Jing
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: PF-1214 USN
; CURRENT APPLICATION NUMBER: US/10/491,183
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/US02/31096
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,388
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/328,979
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/346,034
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/348,284
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/338,048
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/332,340
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/340,357
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/387,119
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/368,799
; PRIOR FILING DATE: 2002-03-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PERL Program
; SEQ ID NO 16
; LENGTH: 169
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7500495CD1
; US-10-491-183-16

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Query Match          69.0%; Score 573; DB 5; Length 169;
Best Local Similarity 100.0%; Pred. No. 4.7e-56;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 50 KTHLPGFVQABALAKGVVAVCLSVNDAPVTGEGRAHKAEGKVRLLADPTGAFGKET 109
DB 57 KTHLPGFVQABALAKGVVAVCLSVNDAPVTGEGRAHKAEGKVRLLADPTGAFGKET 116
QY 110 DILLDDSLVSIIGNRLKRFPSNVQDGIYKALNVEPDGTGLTCSLAPNTISQL 162
DB 117 DILLDDSLVSIIGNRLKRFPSNVQDGIYKALNVEPDGTGLTCSLAPNTISQL 169

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Search completed: February 21, 2006, 22:00:57
 Job time : 169 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:58:17 ; Search time 18 Seconds

(without alignments)
128.157 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830
Sequence: 1 MAPKVGDAIPAVEVEFEGEP.....VEPDGTGLTCSLAPNIIISQL 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 108093 seqs, 14239677 residues

Total number of hits satisfying chosen parameters: 108093

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCF_NEW_PUB pep:*
5: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	214	6	US-10-878-556A-183
2	252.5	30.4	267	6	US-10-467-657-5556
3	107	12.9	187	7	US-11-058-926-22
4	97	11.7	188	7	US-11-058-926-24
5	96	11.6	271	6	US-10-821-234-1419
6	90.5	10.9	257	6	US-10-642-272A-6
7	89.5	10.8	256	6	US-10-642-272A-4
8	89	10.7	206	6	US-10-821-234-1038
9	86.5	10.4	257	6	US-10-642-272A-5
10	86	10.4	198	6	US-10-642-272A-28
11	81	9.8	386	6	US-10-467-657-6564
12	79	9.5	193	6	US-10-527-771-6
13	78.5	9.5	442	6	US-10-485-788A-516
14	78.5	9.5	724	7	US-11-126-313-28
15	78.5	9.5	1219	7	US-11-032-236-4
16	77.5	9.3	446	7	US-11-108-172-1121
17	76	9.2	1170	6	US-10-858-730-71
18	75	9.0	105	6	US-10-485-788A-794
19	75	9.0	1495	7	US-11-053-076-176
20	74.5	9.0	1095	7	US-11-019-711-111
21	74	8.9	1588	7	US-11-052-554A-280
22	71	8.6	164	6	US-10-793-626-252
23	70.5	8.5	3507	7	US-11-075-185-7
24	69.5	8.4	7968	7	US-11-143-980-49
25	69	8.3	621	7	US-11-098-686-10946

26	69	8.3	1479	7	US-11-019-711-36	Sequence 36, Appl
27	69	8.3	4868	7	US-11-044-111-24	Sequence 24, Appl
28	69	8.3	8695	7	US-11-205-109-15	Sequence 15, Appl
29	68.5	8.3	509	7	US-11-098-686-10996	Sequence 10996, A
30	68	8.2	165	6	US-10-454-437-172	Sequence 172, Appl
31	68	8.2	1571	7	US-11-052-554A-2	Sequence 2, Appl
32	68	8.2	7102	7	US-11-143-980-48	Sequence 48, Appl
33	67.5	8.1	365	6	US-10-454-437-394	Sequence 394, Appl
34	67	8.1	4060	6	US-10-922-232B-55	Sequence 55, Appl
35	67	8.1	6738	6	US-10-922-232B-56	Sequence 56, Appl
36	66.5	8.0	3073	7	US-11-143-980-50	Sequence 50, Appl
37	66.5	8.0	5712	7	US-11-143-980-47	Sequence 47, Appl
38	66	8.0	284	6	US-10-485-517-326	Sequence 326, Appl
39	66	8.0	371	6	US-10-467-657-1926	Sequence 1926, Appl
40	65.5	7.9	95	6	US-10-485-788A-659	Sequence 659, Appl
41	65.5	7.9	95	7	US-11-053-076-22	Sequence 22, Appl
42	65.5	7.9	177	6	US-10-980-388-95	Sequence 95, Appl
43	65.5	7.9	239	7	US-11-194-246-304	Sequence 304, Appl
44	65.5	7.9	257	6	US-10-467-657-5876	Sequence 5876, Appl
45	65.5	7.9	257	6	US-10-467-657-7488	Sequence 7488, Appl

ALIGNMENTS

RESULT 1
US-10-878-556A-183
; Sequence 183, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 183
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/pdx5_human
; DATABASE ENTRY DATE: 1993-04-01
US-10-878-556A-183

Query Match 100.0%; Score 830; DB 6; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFGKGGVLFPGVGAFTPGSKTHLPGFVEQA 60
DB 53 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFGKGGVLFPGVGAFTPGSKTHLPGFVEQA 112
QY 61 EALKAGQVAVACSVNDAFTYTGEGRAHKAEGKRVRLADPTGAFGKETDLDLDSIVSI 120
DB 113 EALKAGQVAVACSVNDAFTYTGEGRAHKAEGKRVRLADPTGAFGKETDLDLDSIVSI 172
QY 121 FGNRLKRFPSNVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 162
DB 173 FGNRLKRFPSNVVDGIVKALNVBPDGTGLTCSLAPNIIISQL 214

RESULT 2
US-10-467-657-5556
; Sequence 5556, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta

```

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMin99, version 1.04
; SEQ ID NO 5556
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5556

Query Match          30.4%; Score 252.5; DB 6; Length 267;
Best Local Similarity 38.5%; Pred. No. 8.6e-19;
Matches 57; Conservative 28; Mismatches 56; Indels 7; Gaps 5;

Qy      5 KYGDALPAVEVE---GEGDNKYNLAELFKGKKGVLFEGVGAFTPGCSKTHLPGFVEQAE 61
      28 RRGQKPSV-VFTRRGDVMKOVSTDLFKGKKVVVFSLPGAFPTCSSHLPRVNEELG 86
Db
Qy      62 ALKAGVQVACLVDNDAFVTGEMGRABKGVRLADPTGAFGKETDLLDDSLVSIF 121
      87 AFKENGVDAICCVSVNDTFVNNAMA-AEESDNIYIMPDNGEFTEGMGLVGEKEDIG-F 144
Db
Qy      122 GNRRLKFSMVVODGIVKALNVEPDGTG 149
      145 G-KRSWRISMLVNDGVEMFIEEPBPG 171
Db

RESULT 3
US-11-058-926-22
; Sequence 22, Application US/11058926
; Publication No. US20060030022A1
; GENERAL INFORMATION:
; APPLICANT: BECKWITH, JONATHAN
; APPLICANT: ASLUND, FREDRIK
; APPLICANT: BESSETTE, PAUL H.
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: RITZ, DANIEL
; APPLICANT: LIM, JACKIE EUN-AH
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
; FILE REFERENCE: HMV-052.01
; CURRENT APPLICATION NUMBER: US/11/058,926
; CURRENT FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: US/09/679,705
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/157,770
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/163,939
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/166,044
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-058-926-22

Query Match          12.9%; Score 107; DB 7; Length 187;
Best Local Similarity 28.6%; Pred. No. 0.00056;
Matches 36; Conservative 22; Mismatches 56; Indels 12; Gaps 5;

Qy      31 KKKGGLFGVGPAGFTPGCSKTHLPGFVEQAEALKAGVQVACLVDNDAFVTGEMGRABK 90
      30 EGRWSVFFPYADPTFVC-PTELGVDADHYEELQKLGVDVYA-VSTDTHFTKAMHSSE 87
Db
Qy      91 AEGKVR--LLADPTGAFGKETDLLDDSLVSIFGNRLKFSMVVQ-DGIVKALNVEPDG 147
      145 G-KRSWRISMLVNDGVEMFIEEPBPG 171
Db
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Db      88 TIAIKVAMIGDPTGALTRNFDNREDEGLA-----DRATFVVDPGIIGIIEVTAEG 140
Qy      148 TGLTCS 153
Db      141 IGRDAS 146

RESULT 4
US-11-058-926-24
; Sequence 24, Application US/11058926
; Publication No. US20060030022A1
; GENERAL INFORMATION:
; APPLICANT: BECKWITH, JONATHAN
; APPLICANT: ASLUND, FREDRIK
; APPLICANT: BESSETTE, PAUL H.
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: RITZ, DANIEL
; APPLICANT: LIM, JACKIE EUN-AH
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
; FILE REFERENCE: HMV-052.01
; CURRENT APPLICATION NUMBER: US/11/058,926
; CURRENT FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: US/09/679,705
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/157,770
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/163,939
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/166,044
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-058-926-24

Query Match          11.7%; Score 97; DB 7; Length 188;
Best Local Similarity 28.6%; Pred. No. 0.0061;
Matches 34; Conservative 20; Mismatches 53; Indels 12; Gaps 5;

Qy      38 FGVPAGFTPGCSKTHLPGFVEQAEALKAGVQVACLVDNDAFVTGEMGRABKAEKVR- 96
      38 FFPYADPTFVC-PTELGVDADHYEELQKLGVDVYA-VSTDTHFTKAMHSSETIAIKY 95
Db
Qy      97 -LLADPTGAFGKETDLLDDSLVSIFGNRLKFSMVVQ-DGIVKALNVEPDGTGLTCS 153
      96 AMIGDPTGALTRNFDNREDEGLA-----DRATFVVDPGIIGIIEVTAEGIGRDAS 147
Db

RESULT 5
US-10-821-234-1419
; Sequence 1419, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andamant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1419
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
```



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; CURRENT APPLICATION NUMBER: US/10/642,272A
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: PCT/JP02/01358
; PRIOR FILING DATE: 2001-02-18
; PRIOR APPLICATION NUMBER: JP 41003/2001
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-642-272A-5

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```

Query Match          10.4%; Score 86.5; DB 6; Length 257;
Beet Local Similarity 27.7%; Pred. No. 0.11;
Matches 33; Conservative 22; Mismatches 51; Indels 13; Gaps 4;

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```

QY 30 FKGKGVLPFGVPGAFPPGCKTHLPGFVEQAEALKAKGVVACLSVNDAPVTGEGRAH 89
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 91 FKGKVLVLFYFLDFTFVC-PTEIYAFSDKANEFHDVNEEVA-VSDSHFSLAMINTP 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 90 KAEG-----KVLADPTGAFGKETDLDLSDLSVIFGNRLKRFSSMVVQDGIKALNV 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 149 AKNGGLGHMNTILSDLTQISRVDYGVLLSAGIALRG-----LFIIDPNCVIXKLSV 201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 10

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US-10-642-272A-28
; Sequence 28, Application US/10642272A
; Publication No. US20050277606A1
; GENERAL INFORMATION:
; APPLICANT: Hattori, Fumiyuki
; APPLICANT: Sugimura, Keiichi
; APPLICANT: Futaya, Mayumi
; TITLE OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
; FILE REFERENCE: 58777.000012
; CURRENT APPLICATION NUMBER: US/10/642,272A
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: PCT/JP02/01358
; PRIOR FILING DATE: 2001-02-18
; PRIOR APPLICATION NUMBER: JP 41003/2001
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-642-272A-28

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```

Query Match          10.4%; Score 86; DB 6; Length 198;
Beet Local Similarity 25.4%; Pred. No. 0.089;
Matches 32; Conservative 27; Mismatches 53; Indels 14; Gaps 5;

```

```

QY 23 KVNLAELFGKGVLPFGVPGAFPPGCKTHLPGFVEQAEALKAKGVVACLSVNDAPVT 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27 EKLSD-YGKKTVLFFYFLDFTFVC-PTEIYAFSHADPKLGEVVG-VSDSQFTH 83
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 83 GEMGRAHKAEG-----KVLADPTGAFGKETDLDLSDLSVIFGNRLKRFSSMVVQDGI 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 84 LAMINTPRKEGGLGPLNIPVLADVTSLSQNGVGLKNDGIAVVG-----LFIIDAKGV 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 138 VKALNV 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 138 LKQITV 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 11
US-10-467-657-6564
; Sequence 6564, Application US/10467657
; Publication No. US20050260581A1

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; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6564
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6564

```

```

Query Match          9.8%; Score 81; DB 6; Length 386;
Beet Local Similarity 26.6%; Pred. No. 0.72;
Matches 29; Conservative 15; Mismatches 41; Indels 24; Gaps 3;

```

```

QY 55 FVEQAEALKAKGVVACLSVNDAPVTGEGRAHKAEGKVLADPTGAFGKETD----- 110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 GFINNIVKFGIGVSRVSPDIN-----EWKAIVKANTKLLFETPENPIGEVADLEAL 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 111 -----LLDSDLSVIFGNRLKRFSSMVVQDGIKALNVDPDGTG 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 169 AELAHGIALLVNDNLSLPVGSQPLKRGADISVSATKAI-----DGHG 213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 12

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US-10-527-771-6
; Sequence 6, Application US/10527771
; Publication No. US20050271683A1
; GENERAL INFORMATION:
; APPLICANT: University Gent
; TITLE OF INVENTION: Ostertagia vaccine
; FILE REFERENCE: 2002-015
; CURRENT APPLICATION NUMBER: US/10/527,771
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 10/243,319
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Ostertagia ostertagi
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (72)..(72)
; OTHER INFORMATION: The xaa at location 72 stands for Asn, or Thr.
US-10-527-771-6

```

```

Query Match          9.5%; Score 79; DB 6; Length 193;
Beet Local Similarity 26.4%; Pred. No. 0.46;
Matches 33; Conservative 21; Mismatches 57; Indels 14; Gaps 5;

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QY 24 VNLAELFGKGVLPFGVPGAFPPGCKTHLPGFVEQAEALKAKGVVACLSVNDAPVTG 83
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23 VKLSD-YGKKTVLFFYFLDFTFVC-PTEIYAFSDRVEFPKKIDAAVLAC-SXDSVFSHL 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 EWRHAHKAEG-----KVLADPTGAFGKETDLDLSDLSVIFGNRLKRFSSMVVQDGI 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 80 AMINTPRKGGIGDMNIPVLADVTNQLAKDYGVLLKEDGIAVVG-----LFIIDPKGIL 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 139 KALNV 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 134 KQITV 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



```
RESULT 13
US-10-485-788A-516
; Sequence 516, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-0032005
; CURRENT APPLICATION NUMBER: US/10/485,788A
; PRIORITY FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 516
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: post-synaptic desensitly protein 95 (PSD95)
; OTHER INFORMATION: Construct (N-P3) aa 1 - aa 442
US-10-485-788A-516

Query Match          9.5%; Score 78.5; DB 6; Length 442;
Best Local Similarity 27.3%; Pred. No. 1.6;
Matches 39; Conservative 19; Mismatches 40; Indels 45; Gaps 9;

Cy 20 PGNKVNLAELFKGKGGVLFVGAFPTPGCSKTHLPGFVEQAALAKAGVQVVAACLSVND 79
Db 197 PAKRMEIKLIKPGKGLGFSIAG-----GVGNQHIFG-----DNSI 232
Cy 80 FVTG--EMGRAHKAEGKV---RLADPTGAFGKETDLLDLSVIFGNRLKRFSMNV 133
Db 233 YVTKIIEGGAHAK-DGRLOIGDKILA--VNSVGL-EVMEHDAVA-----LKNTYDVV 282
Cy 134 QDGIVKALNVEPDGTGLTCSLAP 156
Db 283 YLKVAK-----PSNAVYLSDSYAP 300

RESULT 14
US-11-126-313-28
; Sequence 28, Application US/11126313
; Publication No. US2005028489A1
; GENERAL INFORMATION:
; APPLICANT: Hirsch, Joel
; TITLE OF INVENTION: VOLTAGE-DEPENDENT CALCIUM CHANNEL BETA SUBUNIT FUNCTIONAL CORE
; FILE REFERENCE: P-6758-US
; CURRENT APPLICATION NUMBER: US/11/126,313
; PRIORITY FILING DATE: 2005-05-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-126-313-28

Query Match          9.5%; Score 78.5; DB 7; Length 724;
Best Local Similarity 27.3%; Pred. No. 3;
Matches 39; Conservative 19; Mismatches 40; Indels 45; Gaps 9;

Cy 20 PGNKVNLAELFKGKGGVLFVGAFPTPGCSKTHLPGFVEQAALAKAGVQVVAACLSVND 79
Db 197 PAKRMEIKLIKPGKGLGFSIAG-----GVGNQHIFG-----DNSI 232
```

```
Db 154 PAKRMEIKLIKPGKGLGFSIAG-----GVGNQHIFG-----DNSI 189
Cy 80 FVTG--EMGRAHKAEGKV---RLADPTGAFGKETDLLDLSVIFGNRLKRFSMNV 133
Db 190 YVTKIIEGGAHAK-DGRLOIGDKILA--VNSVGL-EVMEHDAVA-----LKNTYDVV 239
Cy 134 QDGIVKALNVEPDGTGLTCSLAP 156
Db 240 YLKVAK-----PSNAVYLSDSYAP 257

RESULT 15
US-11-032-236-4
; Sequence 4, Application US/11032236
; Publication No. US20050273867A1
; GENERAL INFORMATION:
; APPLICANT: BRULET, PHILIPPE
; APPLICANT: ROGERS, KELLY
; APPLICANT: PICAUD, SANDRINE
; TITLE OF INVENTION: NON-INVASIVE REAL-TIME IN VIVO BIOLUMINESCENCE IMAGING
; FILE REFERENCE: 03495.0328
; CURRENT APPLICATION NUMBER: US/11/032,236
; PRIORITY FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/543,659
; PRIOR FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 1219
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: coding sequence contained in PSDA vector
US-11-032-236-4

Query Match          9.5%; Score 78.5; DB 7; Length 1219;
Best Local Similarity 27.3%; Pred. No. 6.1;
Matches 39; Conservative 19; Mismatches 40; Indels 45; Gaps 9;

Cy 20 PGNKVNLAELFKGKGGVLFVGAFPTPGCSKTHLPGFVEQAALAKAGVQVVAACLSVND 79
Db 154 PAKRMEIKLIKPGKGLGFSIAG-----GVGNQHIFG-----DNSI 189
Cy 80 FVTG--EMGRAHKAEGKV---RLADPTGAFGKETDLLDLSVIFGNRLKRFSMNV 133
Db 190 YVTKIIEGGAHAK-DGRLOIGDKILA--VNSVGL-EVMEHDAVA-----LKNTYDVV 239
Cy 134 QDGIVKALNVEPDGTGLTCSLAP 156
Db 240 YLKVAK-----PSNAVYLSDSYAP 257
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Search completed: February 21, 2006, 22:01:20
Job time : 19 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:46:26 ; Search time 47 Seconds
(without alignments)
284.967 Million cell updates/sec

Title: US-10-686-157-2
Perfect score: 830
Sequence: 1 MAPIKVGDALPAVEVFEGEP.....VEPDGTGLTCLAPNIISQL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	162	2	US-09-486-167A-2
2	830	100.0	214	2	US-08-959-004-1
3	752	90.6	162	2	US-09-486-167A-4
4	364	43.9	125	2	US-09-513-999C-8124
5	355.5	42.8	202	2	US-09-248-796A-16927
6	315	38.0	118	2	US-09-513-999C-6299
7	252.5	30.4	189	2	US-08-959-004-8
8	241.5	29.1	270	2	US-09-540-236-2375
9	213.5	25.7	167	2	US-08-959-004-7
10	194	23.4	166	2	US-09-091-007-4
11	194	23.4	166	2	US-10-109-670-9
12	191	23.0	176	2	US-09-091-097-2
13	191	23.0	176	2	US-10-109-670-8
14	191	23.0	177	2	US-09-091-097-19
15	191	23.0	177	2	US-10-109-670-19
16	176.5	16.4	185	2	US-09-248-796A-20861
17	176.5	16.4	210	2	US-09-248-796A-20862
18	112	13.5	183	2	US-09-107-532A-6874
19	108	13.0	212	2	US-09-540-236-2729
20	107	12.9	187	2	US-09-679-705-22
21	104	12.5	187	2	US-09-489-039A-13465
22	100.5	12.1	157	2	US-09-489-039A-9071
23	100.5	12.1	176	2	US-09-902-540-12942
24	100.5	12.1	174	2	US-09-902-540-16718
25	99.5	12.0	157	2	US-09-543-681A-8014
26	99	11.9	205	2	US-09-543-681A-817
27	97.5	11.7	214	2	US-09-543-681A-6147

28	97	11.7	188	2	US-09-679-705-24	Sequence 24, Appl
29	97	11.7	196	2	US-09-538-092-593	Sequence 593, App
30	96	11.6	271	1	US-08-467-265-2	Sequence 2, Appl
31	96	11.6	271	2	US-08-467-265-2	Sequence 2, Appl
32	96	11.6	271	2	US-09-407-891-2	Sequence 1, Appl
33	96	11.6	271	2	US-09-375-907-1	Sequence 1, Appl
34	96	11.6	271	2	US-09-538-092-1298	Sequence 1298, Ap
35	95	11.4	218	2	US-09-248-796A-15000	Sequence 15000, A
36	94.5	11.4	167	2	US-09-902-540-13018	Sequence 13018, A
37	94.5	11.4	199	2	US-09-375-907-2	Sequence 2, Appl
38	94.5	11.4	199	2	US-09-375-907-4	Sequence 4, Appl
39	94	11.3	196	2	US-09-134-001C-4601	Sequence 4601, Ap
40	93.5	11.3	199	1	US-08-299-162A-2	Sequence 2, Appl
41	93.5	11.3	199	1	US-08-467-265-14	Sequence 14, Appl
42	93.5	11.3	199	2	US-08-467-265-14	Sequence 14, Appl
43	93.5	11.3	199	2	US-09-407-891-14	Sequence 14, Appl
44	93.5	11.3	199	2	US-09-538-092-1277	Sequence 1277, Ap
45	91	11.0	195	2	US-10-197-220-101	Sequence 101, App

ALIGNMENTS

```

RESULT 1
US-09-486-167A-2
Sequence 2, Application US/09486167A
Patent No. 6759194
GENERAL INFORMATION:
APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE SEQUENCE ENCODING SAI
TITLE OF INVENTION: AND THEIR USES IN THE DIAGNOSTIC AND/OR THE TREATMENT OF LUNG IN
FILE REFERENCE: VANM143.001A
CURRENT APPLICATION NUMBER: US/09/486.167A
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-486-167A-2

Query Match      100.0%; Score 830; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.6e-93;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAPIKVGDALPAVEVFEGEPGNKRVLAELFGKKGVLFGVGAFTPGCGSKTHLPGFVEQA 60
      |||
DB      1 MAPIKVGDALPAVEVFEGEPGNKRVLAELFGKKGVLFGVGAFTPGCGSKTHLPGFVEQA 60
      |||

QY      61 EALRAKGVVAVACISVNDAPFTGEGRAHKAEGKRVLLADPTGAFGKETDILLDDSLVSI 120
      |||
DB      61 EALRAKGVVAVACISVNDAPFTGEGRAHKAEGKRVLLADPTGAFGKETDILLDDSLVSI 120
      |||

QY      121 FGNRLKRFKFSNVVDGTYKALNVBPDTGTLTCLAPNIISQL 162
      |||
DB      121 FGNRLKRFKFSNVVDGTYKALNVBPDTGTLTCLAPNIISQL 162
      |||

RESULT 2
US-08-959-004-1
Sequence 1, Application US/08959004
Patent No. 6197543
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Ial, Preeti
APPLICANT: Shah, Parvi
APPLICANT: Kaser, Matthew
TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE

```

```
/ TITLE OF INVENTION: PROTEINS
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/959,004
/ FILING DATE: Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0414 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 214 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BRA1UTY01
/ CLONE: 743725
/ US-08-959-004-1

Query Match      100.0%; Score 830; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.5e-93;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEVEFEGEPGNKNVLAELFKGKGGVLFQVPGAFTPGCSKTHLPGFVEQA 60
    |||||
DB 53 MAPIKVGDAIPAVEVEFEGEPGNKNVLAELFKGKGGVLFQVPGAFTPGCSKTHLPGFVEQA 112
    |||||

QY 61 EALKAKGVQVVAACLSVNDAFVTGEMGRARAKAGKVRLLADPTGAFGKETDILLDDSLVSI 120
    |||||
DB 113 EALKAKGVQVVAACLSVNDAFVTGEMGRARAKAGKVRLLADPTGAFGKETDILLDDSLVSI 172
    |||||

QY 121 FGNRLKRPMSVWVODGIYKALNVEPDGTLTCSLAPNIISQL 162
    |||||
DB 173 FGNRLKRPMSVWVODGIYKALNVEPDGTLTCSLAPNIISQL 214
    |||||

RESULT 3
US-09-486-167A-4
/ Sequence 4; Application US/09486167A
/ Patent No. 6759194
/ GENERAL INFORMATION:
/ APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
/ TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE SEQUENCE ENCODING SAI
/ TITLE OF INVENTION: AND THEIR USES IN THE DIAGNOSTIC AND/OR THE TREATMENT OF LUNG IN
/ FILE REFERENCE: VANM143.001A
/ CURRENT APPLICATION NUMBER: US/09/486,167A
/ CURRENT FILING DATE: 2000-08-15
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
```

```
/ LENGTH: 162
/ TYPE: PRT
/ ORGANISM: Rattus rattus
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 17
/ OTHER INFORMATION: Glu or Gly
/ NAME/KEY: Modified-site
/ LOCATION: 63
/ OTHER INFORMATION: Leu or Pro
/ NAME/KEY: Modified-site
/ LOCATION: 79
/ OTHER INFORMATION: Ala or Val
/ US-09-486-167A-4

Query Match      90.6%; Score 752; DB 2; Length 162;
Best Local Similarity 88.9%; Pred. No. 5.9e-84;
Matches 144; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEVEFEGEPGNKNVLAELFKGKGGVLFQVPGAFTPGCSKTHLPGFVEQA 60
    |||||
DB 1 MAPIKVGDTIPSEVFEFGEPGNKNVLAELFKGKGGVLFQVPGAFTPGCSKTHLPGFVEQA 60
    |||||

QY 61 EALKAKGVQVVAACLSVNDAFVTGEMGRARAKAGKVRLLADPTGAFGKETDILLDDSLVSI 120
    |||||
DB 61 GAXKAKGAQVVAACLSVNDXFTVAGMGRARAKAGKVRLLADPTGAFGKETDILLDDSLVSI 120
    |||||

QY 121 FGNRLKRPMSVWVODGIYKALNVEPDGTLTCSLAPNIISQL 162
    |||||
DB 121 FGNRLKRPMSVWIDRGVVAALNVEPDGTLTCSLAPNIISQL 162
    |||||

RESULT 4
US-09-513-999C-8124
/ Sequence 8124; Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclet, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59. US2. REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 8124
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 80
/ OTHER INFORMATION: Xaa=Asp or Glu
/ US-09-513-999C-8124

Query Match      43.9%; Score 364; DB 2; Length 125;
Best Local Similarity 98.6%; Pred. No. 1.5e-36;
Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEVEFEGEPGNKNVLAELFKGKGGVLFQVPGAFTPGCSKTHLPGFVEQA 60
    |||||
DB 53 MAPIKVGDAIPAVEVEFEGEPGNKNVLAELFKGKGGVLFQVPGAFTPGCSKTHLPGFVEQA 112
    |||||

QY 61 EALKAKGVQVVA 72
    |||||
DB 113 EALKAKGVQVVA 124
    |||||

RESULT 5
```

US-09-248-796A-16927
 ; Sequence 16927, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; PRIOR FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 16927
 ; LENGTH: 202
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-16927

Query Match 42.8%; Score 355.5; DB 2; Length 202;
 Best Local Similarity 44.1%; Pred. No. 3.3e-35;
 Matches 71; Conservative 25; Mismatches 60; Indels 5; Gaps 2;

QY 4 IKVGDALPVEFEGEPGNKVNLAELFKGKKGVLRFGAFPGCKTHLPGEVQAL 63
 Db 43 VSIGDKVATVFEESPGNDINLAETASGKITLGVGASPSACSHVPEYINIAF 102
 QY 64 KAKGVVAVCLSVNDAFVTEGWR--AKKAGKVRLLADPTGAFGKETDLLDLSVSI 120
 Db 103 NDKGVQRFVAVNDPFTTKAMGEQLLSVAGQIRFADSTGATTKELDLFDR--KA 160
 QY 121 FGNRLKRFMSVVDGIVKALNVEPDGTGLTCSLAPNISQ 161
 Db 161 FGNRSKRVALIIEGKVKSVFVEDNTSVSAQKVLER 201

RESULT 6
 US-09-513-999C-6299
 ; Sequence 6299, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59, US2, REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 6299
 ; LENGTH: 118
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-513-999C-6299

Query Match 38.0%; Score 315; DB 2; Length 118;
 Best Local Similarity 80.7%; Pred. No. 1.4e-30;
 Matches 67; Conservative 0; Mismatches 6; Indels 10; Gaps 1;

QY 83 GEM-----GRAHRAEGKVRLLADPTGAFGKETDLLDLSVIFGNRLKRFPMV 132
 Db 36 GEMAGGVRSFRAAAAPIKVRLADPTGAFGKETDLLDLSVIFGNRLKRFPMV 95
 QY 133 VODGIVKALNVEPDGTGLTCSLA 155
 Db 96 VODGIVKALNVEPDGTGLTCSLA 118

RESULT 7
 US-08-959-004-8
 ; Sequence 8, Application US/08959004
 ; Patent No. 6197543
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Kaser, Matthew
 ; TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE
 ; TITLE OF INVENTION: PROTEINS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Inocyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/959,004
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0414 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 189 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1652858
 US-08-959-004-8

Query Match 30.4%; Score 252.5; DB 2; Length 189;
 Best Local Similarity 39.8%; Pred. No. 1.3e-22;
 Matches 64; Conservative 27; Mismatches 53; Indels 17; Gaps 7;

QY 8 DALPVEYF-----EGBPG-----NKVNLAELFKGKKGVLRFGVPAFTGCKSTHLP 55
 Db 4 ERVPSV-VFKTRVDESGPGNPYRWEDKTEQIFGKKVLLFSLPGAFTTCSSNHLPR 62
 QY 56 FVEQAEALKAKGVVAVCLSVNDAFVTEGWRGAHRAEGKVRLLADPTGAFGKETDLLD 115
 Db 63 YEQIFEEQALGVDDITCLSVNDAFVTEGWRQAGAD-KVLLDPDGNGEFTRRKGMVVK 121
 QY 116 SLVSI FGNRLKRFMSVVDGIVKALNVEPDGTGLTCSLAP 156
 Db 122 SNLG-FGMRSM-RYSMFVNDGKIKMFIEPE-FGDNCPVDP 159

RESULT 8
 US-09-540-236-2375
 ; Sequence 2375, Application US/09540236

/ Patent No. 6673910
/ GENERAL INFORMATION:
/ APPLICANT: Gary L. Breton et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
/ FILE REFERENCE: 2709.2005-001
/ CURRENT APPLICATION NUMBER: US/09/540,236
/ CURRENT FILING DATE: 2000-04-04
/ NUMBER OF SEQ ID NOS: 3840
/ SEQ ID NO 2375
/ LENGTH: 270
/ TYPE: PRT
/ ORGANISM: M.catarhalis
US-09-540-236-2375

Query Match 29.1%; Score 241.5; DB 2; Length 270;
Best Local Similarity 39.0%; Pred. No. 4.7e-21;
Matches 57; Conservative 26; Mismatches 56; Indels 7; Gaps 5;

QY 7 GDAIPAVEYEGEPGRK--VNIAELFKGKGVLFVGPAPTPGCSKTHLPGVBOBAL 63
DB 29 GQKVPFA-VFTRQGDQWVDVNTDELFSGKVVVPSLPFAFTPTCSSTHLPKRNELADEF 87
QY 64 KAKGVQVACLSVNDFAVTVGEMGRAHKAEGVRLADPTGAFGKETDLLLDDSLVSIFGN 123
DB 88 KKLGIIDILCVSGVNDTFVNNAMADQESD-KITLIPDNGGFTGKGNRLVSKEDLG-FG- 144
QY 124 RLKRFMSVVOGIVKALNVEPDGTG 149
DB 145 KRSWYSMLVDGMIVKIFDEPKDG 170

RESULT 9
US-08-959-004-7
Sequence 7, Application US/08959004
Patent No. 6197543

/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Yue, Henry
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Lal, Preeti
/ APPLICANT: Shah, Purni
/ APPLICANT: Kaser, Matthew
/ TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE
/ TITLE OF INVENTION: PROTEINS
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/959,004
/ FILING DATE: Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0414 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX:

/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 167 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 170899
US-08-959-004-7

Query Match 25.7%; Score 213.5; DB 2; Length 167;
Best Local Similarity 35.3%; Pred. No. 6.3e-18;
Matches 60; Conservative 31; Mismatches 68; Indels 11; Gaps 6;

QY 1 MAPIVGAIPIAV-BVF-----EGPRGNKVNLAELFKGKGVLFVGPAPTPGCSKTHLP 54
DB 1 MAPIRGRFPPTDVIYIIPPEGGPG-PLBLSKRVKTKRVVSVPAFTPTCTEQHLP 59
QY 55 GFVEQAEALKAKGVQVACLSVNDFAVTVGEMGRAHKAEG-KVRLADPTGAFGKETD 112
DB 60 GYIKLPLRLSKGVDFVLVISQNDPFVLKKGKKELGADAKKLVVSDPNLKTCKGST 119
QY 113 LDDSLVSIFGNRLKRFMSVVOGIVKALNVEPDGTGLTCSLAPNIIISQL 162
DB 120 IDLSAIGL-GTRSGRLALIVNRSGIVEYAAIE-NGGEVDVSTAQKIIAKL 167

RESULT 10
US-09-091-097-4
Sequence 4, Application US/09091097
Patent No. 6432407

/ GENERAL INFORMATION:
/ APPLICANT: TAKESAKO, KAZUTOH
/ APPLICANT: OKADO, TAKASHI
/ APPLICANT: YAGIHARA, TOMOKO
/ APPLICANT: KURODA, MASANOBU
/ APPLICANT: ONISHI, YOSHIMI
/ APPLICANT: KATO, IKUNOSHIN
/ APPLICANT: AKIYAMA, KAZUO
/ APPLICANT: YASUDA, HIROSHI
/ APPLICANT: YAMAGUCHI, HIDEYO
/ TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
/ TITLE OF INVENTION: MALTASEZIN
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
/ STREET: PO BOX 747
/ CITY: FALLS CHURCH
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22040-0747
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/091,097
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WEINER, MARC S.
/ REGISTRATION NUMBER: 32,181
/ REFERENCE/DOCKET NUMBER: 1422-0346P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-205-8000
/ TELEFAX: 703-205-8050
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 166 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-091-097-4

Query Match 23.4%; Score 194; DB 2; Length 166;

Best Local Similarity 35.5%; Pred. No. 1.5e-15;
Matches 49; Conservative 21; Mismatches 58; Indels 10; Gaps 3;

QY 28 ELFGKGGVLFVPGAFPTGCGSKTHLPGFVEQAEALAKAGVQVAVCLSVNDAFVTEGMR 87

DB 36 ERMKGGKVVIVAVPAFTPTCTANHVPPYVEKIQELKSGKGVDEVVVISANDPVLAMGI 95

QY 88 AHKAGKVRLLADPTGAFGKETDILLDSLVISFGNRRLLKFSMVVQDGIYKALNV---E 144

DB 96 TEHADNLTFAQDVNCEFSKHNATLD--LSKGMGLRTARYALANDLKVEYFGIDEGE 153

QY 145 PDGTLTCSLAPNIISQL 162

DB 154 PKQ-----SSAATVLSKL 166

RESULT 11

US-10-109-670-9
Sequence 9, Application US/10109670

Patent No. 6911208

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH et al.

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA

FILE REFERENCE: 1422-0523P

CURRENT APPLICATION NUMBER: US/10/109,670

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 9

LENGTH: 166

TYPE: PRT

ORGANISM: Malassezia furfur

US-10-109-670-9

Query Match 23.4%; Score 194; DB 2; Length 166;

Best Local Similarity 35.5%; Pred. No. 1.5e-15;
Matches 49; Conservative 21; Mismatches 58; Indels 10; Gaps 3;

QY 28 ELFGKGGVLFVPGAFPTGCGSKTHLPGFVEQAEALAKAGVQVAVCLSVNDAFVTEGMR 87

DB 36 ERMKGGKVVIVAVPAFTPTCTANHVPPYVEKIQELKSGKGVDEVVVISANDPVLAMGI 95

QY 88 AHKAGKVRLLADPTGAFGKETDILLDSLVISFGNRRLLKFSMVVQDGIYKALNV---E 144

DB 96 TEHADNLTFAQDVNCEFSKHNATLD--LSKGMGLRTARYALANDLKVEYFGIDEGE 153

QY 145 PDGTLTCSLAPNIISQL 162

DB 154 PKQ-----SSAATVLSKL 166

RESULT 12

US-09-091-097-2
Sequence 2, Application US/09091097

Patent No. 6432407

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH

APPLICANT: OKADO, TAKASHI

APPLICANT: YAGIHARA, TOMOKO

APPLICANT: KURODA, MASANOBU

APPLICANT: ONISHI, YOSHIMI

APPLICANT: KATO, IKUNOSHIN

APPLICANT: AKIYAMA, KAZUO

APPLICANT: YAMAGUCHI, HIDEYO

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN

MALASSEZIA

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: PO BOX 747
CITY: FALLS CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,097

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S.

REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 1422-0346P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 176 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-091-097-2

Query Match 23.0%; Score 191; DB 2; Length 176;

Best Local Similarity 35.8%; Pred. No. 3.9e-15;
Matches 43; Conservative 21; Mismatches 54; Indels 2; Gaps 2;

QY 30 FKGGKGVLFVPGAFPTGCGSKTHLPGFVEQAEALAKAGVQVAVCLSVNDAFVTEGMR 89

DB 45 WKGGKVVIVAVPAFTPTCTANHVPPYVEKIQELKSGKGVDEVVVISANDPVLAMGI 104

QY 90 KAGKVRLLADPTGAFGKETDILLDSLVISFGNRRLLKFSMVVQDGIYKALNVDPDGTG 149

DB 105 NAKQKVPFADIDIALFSAKALGATIDLS-AKHFG-ERTARYALIIDDKKIYDFASDEBDTG 162

RESULT 13

US-10-109-670-8
Sequence 8, Application US/10109670

Patent No. 6911208

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH et al.

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA

FILE REFERENCE: 1422-0523P

CURRENT APPLICATION NUMBER: US/10/109,670

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 8

LENGTH: 176

TYPE: PRT

ORGANISM: Malassezia furfur

US-10-109-670-8

Query Match 23.0%; Score 191; DB 2; Length 176;

Best Local Similarity 35.8%; Pred. No. 3.9e-15;
Matches 43; Conservative 21; Mismatches 54; Indels 2; Gaps 2;

QY 30 FKGGKGVLFVPGAFPTGCGSKTHLPGFVEQAEALAKAGVQVAVCLSVNDAFVTEGMR 89

DB 45 WKGGKVVIVAVPAFTPTCTANHVPPYVEKIQELKSGKGVDEVVVISANDPVLAMGI 104

QY 90 KAGKVRLLADPTGAFGKETDILLDSLVISFGNRRLLKFSMVVQDGIYKALNVDPDGTG 149

DB 105 NAKQKVPFADIDIALFSAKALGATIDLS-AKHFG-ERTARYALIIDDKKIYDFASDEBDTG 162

RESULT 14


```

US-09-091-097-19
: Sequence 19, Application US/09091097
: Patent No. 6432407
: GENERAL INFORMATION:
:   APPLICANT: TAKESAKO, KAZUTOH
:   APPLICANT: OKADO, TAKASHI
:   APPLICANT: YAGIHARA, TOMOKO
:   APPLICANT: KURODA, YASUOBU
:   APPLICANT: ONISHI, YOSHIMI
:   APPLICANT: KATO, IKUNOSHIN
:   APPLICANT: AKIYAMA, KAZUO
:   APPLICANT: YASUEDA, HIROSHI
:   APPLICANT: YAMAGUCHI, HIDEYO
:   TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
:   MALASSEZIA
:   NUMBER OF SEQUENCES: 58
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
:     STREET: PO BOX 747
:     CITY: FALLS CHURCH
:     STATE: VA
:     COUNTRY: USA
:     ZIP: 22040-0747
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patent in Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/09/091,097
:     FILING DATE:
:     CLASSIFICATION: 424
:     ATTORNEY/AGENT INFORMATION:
:       NAME: WEINER, MARC S.
:       REGISTRATION NUMBER: 32,181
:       REFERENCE/DOCKET NUMBER: 1422-0346P
:       TELECOMMUNICATION INFORMATION:
:         TELEPHONE: 703-205-8000
:         TELEFAX: 703-205-8050
:       INFORMATION FOR SEQ ID NO: 19:
:         SEQUENCE CHARACTERISTICS:
:           LENGTH: 177 amino acids
:           TYPE: amino acid
:           TOPOLOGY: linear
:         MOLECULE TYPE: peptide
:   US-09-091-097-19
:
: Query Match      23.0%; Score 191; DB 2; Length 177;
: Best Local Similarity 35.8%; Pred. No. 3,9e-15;
: Matches 43; Conservative 21; Mismatches 54; Indels 2; Gaps 2
:
: Oy      30 EKGGKGVLPVPGATTPGCGSKTHLPGFYEQEALAKAGYQVYVACLVNDAPFTGEMGRH 89
:      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Db      46 WKGGKVVIVISPGATTPICHOQHIPPVYKRVDELAKGDAYVIVIASNDPFVMAAMGRFN 105
:      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Oy      90 KAGGVRLADPTGAFGKRTDLDLDSLVISIRGNRLKRFMSVVDGIVKALNVEPDGTG 149
:      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Db      106 NAKDKVVFATDIDLAFSKALGATIDLS-AKAFG-ERTARYALITIDNKIVDPASDEGDTG 163
:      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:
: RESULT 15
: US-10-109-670-19
: Sequence 19, Application US/10109670
: Patent No. 6911208
: GENERAL INFORMATION:
:   APPLICANT: TAKESAKO, KAZUTOH et al.
:   TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
:   FILE REFERENCE: 1422-0523P
:   CURRENT APPLICATION NUMBER: US/10/109,670
:   CURRENT FILING DATE: 2002-04-01
:   NUMBER OF SEQ ID NOS: 58
:   SEQ ID NO 19
:   LENGTH: 177

```

```

:      TYPE: PRT
:      ORGANISM: Malassezia furfur
US-10-109-670-19

Query Match          23.0%; Score 191; DB 2; Length 177;
Best Local Similarity 35.8%; Pred. No. 3.9e-15;
Matches 43; Conservative 21; Mismatches 54; Indels 2; Gaps 2

Qy    30 FKGKKGVLFVGPAGFTPGSCSKTHLPGFPEOKALAKKVVAVACLSVDNAFVTGEMGRAH   89
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     46 WKGGKVIVISIPGATPICHOOHTPLVKRDELKAKGVDAVYVASNDPFVMAMGNFN   105
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy     90 KAEKRVRLIADPTGAFGKETDILLDDSLVISIFGNRIKLRFMSNVVDGIVKALNVEPDGTG   149
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     106 NAKDKVVFATIDIALAFSKALGATIDL$-AKHFG-$ERTARVALIIDNKIKVPFASDEGDPTG   163
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Search completed: February 21, 2006, 21:47:47
Job time : 48 secs
```

Search completed: February 21, 2006, 21:47:47
Job time : 48 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:38:52 ; Search time 186 Seconds
(without alignments)
382.685 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPIKVGDPAIPAVEVFEGEP.....VEPDGTGLTCSLAPNIIISQL 162

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	162	2	AAV01079 Human pro
2	830	100.0	162	2	AdJ70346 Human hea
3	830	100.0	205	4	ABBI1403 Human Ali
4	830	100.0	214	2	AAV17388 Human ves
5	830	100.0	214	7	AdJ68964 Human hea
6	830	100.0	214	7	ADM83091 Human ves
7	830	100.0	214	9	ADM08846 Human pro
8	830	100.0	214	9	AdY81123 Human bra
9	830	100.0	214	9	AEAL17061 Alzheim
10	825	99.4	161	7	AdJ70591 Human hea
11	818	98.6	226	5	AAJ78658 Human per
12	777	93.6	226	5	ABP42382 Human ova
13	701	84.5	194	6	ABU00319 Human nov
14	667	80.4	150	4	AAH87638 Human nov
15	573	65.0	169	7	AdC14210 Human enz
16	569	66.6	351	4	ABG20681 Human hum
17	568	68.4	170	6	ABU00321 Human nov
18	498	60.0	137	4	ADG27703 Human nov
19	479	57.7	157	4	ABH63096 Drosophil
20	469.5	56.6	285	4	ABG09401 Novel hum
21	364	43.9	125	3	AAJ04043 Human sec
22	346	41.7	130	5	ABP42342 Human ova
23	315	38.0	118	3	AAJ02218 Human sec
24	310	37.3	162	8	ADM48269 Polypepti

25	310	37.3	248	8	ADX88783 Plant ful
26	294	35.4	162	3	AAJ05212 Arabidops
27	294	35.4	179	3	AAJ05211 Arabidops
28	289.5	34.9	234	8	ADT56507 Plant pol
29	289	34.8	162	3	AAJ10272 Arabidops
30	288	34.7	162	3	AAJ38202 Arabidops
31	288	34.7	162	7	ADL18519 Rice thio
32	288	34.7	162	7	ADJ11372 Rice prot
33	288	34.7	162	7	ADJ11814 Rice prot
34	288	34.7	162	7	ABM90086 Rice abio
35	288	34.7	179	3	AAJ38201 Arabidops
36	286	34.5	162	3	AAJ38958 Arabidops
37	286	34.5	162	3	AAJ11980 Arabidops
38	286	34.5	162	6	ABP81187 Arabidops
39	286	34.5	182	3	AAJ11979 Arabidops
40	280	33.7	162	7	ADL18521 Arabidops
41	277	33.4	162	3	AAJ10252 Arabidops
42	277	33.4	180	3	AAJ10251 Arabidops
43	263	31.7	164	7	ABM89372 Rice abio
44	259.5	31.3	126	3	AAJ38450 Arabidops
45	255	30.7	160	7	ABM90200 Rice abio

ALIGNMENTS

RESULT 1	AAV01079 standard; protein, 162 AA.
ID	AAV01079
AC	AAV01079;
DT	08-JUN-1999 (first entry)
DE	Human bronchoalveolar polypeptide, B18hum.
XX	B18hum; bronchoalveolar protein; peroxisome-associated polypeptide;
XX	lung injury; oxidative stress-related disorder; inflammatory disease;
XX	cardiovascular disease; neurodegenerative disorder; allergic reaction;
XX	amyotrophic lateral sclerosis; apoptosis; high bone mass syndrome;
XX	osteoporosis; osteoporosis-pseudoglioma syndrome; diagnosis;
XX	Bardet-Biedl syndrome 1; therapy4.
OS	Homo sapiens.
XX	FN
XX	W09909054-A2;
XX	PD
XX	25-FEB-1999.
XX	PF
XX	20-AUG-1998; 98MO-BE000124.
XX	PR
XX	20-AUG-1997; 97BE-00000692.
XX	PA
XX	(UWLO-) UNIV CATHOLIQUE LOUVAIN.
XX	(UWMO-) UNIV MONS-HAINAUT.
XX	PI
XX	Knoops B, Hermans C, Bernard A, Wattiez R, Falmagne P;
XX	WPI; 1999-180968/15.
XX	DR
XX	N-PSDB; AAX27965.
XX	PS
XX	Claim 4; Page 33-34; 45P; English.
XX	This sequence is the human bronchoalveolar polypeptide, designated B18hum
XX	of the invention. B18hum is a low molecular weight human, peroxisome-
XX	associated broncho-alveolar polypeptide. A diagnostic device featuring
XX	the polypeptide, polynucleotide and/or inhibitor is useful for in vitro
XX	detection of lung injuries and diseases or oxidative stress-related
XX	diseases and disorders, especially inflammatory diseases. The device is

also useful for monitoring such diseases or disorders in patients or fluid samples. The polypeptide, polynucleotide and inhibitor form pharmaceutical compositions useful in the prevention and/or treatment of these diseases or disorders, especially specific cardio-vascular diseases (e.g. atherosclerosis), neurodegenerative disorders (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral sclerosis, apoptosis and inflammatory reactions, allergic reactions (e.g. asthma, hay fever and eczema), high bone mass syndrome, osteoporosis, osteopetrosis-pseudoglioma syndrome, and Bardet-Biedl syndrome. 1. The polypeptide is also useful as a specific marker of the above diseases or disorders in a wide variety of tissues. The discovery of the peroxisome-associated polypeptide enables the development of diagnosis and treatment of peroxisomal disorders

SQ Sequence 162 AA;

```
Query Match      100.0%; Score 830; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.9e-90;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY 1 MAPIKVGDAI PAVEVEEGRGKVNLAELPKGKKGLPGVPGAFTFGCSKTHLPGFVEQA 60

Db 1 MAPIKVGDAI PAVEVEEGRGKVNLAELPKGKKGLPGVPGAFTFGCSKTHLPGFVEQA 60

QY 61 EALKKAGVAVACLNDVADFTTGEWGRARAKEGKVRLLDPTGAFGKERTDLLDDSLVSI 120

Db 61 EALKKAGVAVACLNDVADFTTGEWGRARAKEGKVRLLDPTGAFGERTDLLDDSLVSI 120

RESULT 2
ADJ70346
ID ADJ70346 standard; protein; 162 AA

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID2152.

KM microchochdial; human; screening assay; diabetes mellitus;
KM Huntington's disease; osteoarthritis;
KM Leber's hereditary optic neuropathy; LHON;
KM mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KM myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KM neuroprotective; neurotropic; antidiabetic; anticonvulsant; antarthritic;
KM osteoporotic; ophthalmological; cytostatic.

Homo sapiens.

PN WO2003087768-A2

PD 23-OCT-2003

PF 04-APR-2003; 2003WO-US010870.

PR 12-APR-2002; 2002US-0372843P
PR 17-JUN-2002; 2002US-0389987P
PR 20-SEP-2002; 2002US-0412418P

PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.

PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM,
PI Warnock DE;

WPI; 2003-845369/78.

PT Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function.

PT comprises detecting a modified polypeptide in a sample and correlating PT with the disease.

PS Claim 1; SEQ ID NO 2152; 180pp; English.

This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERF) or cancer. Accordingly, these compositions have neuroprotective, neurotropic, antidabetic, anticonvulsant, antiarrhythmic, osteopathic, ophthalmological and cyostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

Sequence 162 AA;

Query Match	100.0%;	Score 830;	DB 7;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 4.9e-90;		
Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy MATIRKGDPAI PAVEVEGEPGRKNLAELFGKKGVLVGVGSAFTPGGSKTHLGGFPEQA 60
 Db 1 MATIRKGDPAI PAVEVEGEPGRKNLAELFGKKGVLVGVGSAFTPGGSKTHLGGFPEQA 60
 Oy 61 EALKANGVOVACLSYNDAFVTGEMGRHAKBGRKRLIADPTGAFGKETDILLDDSLVSI 120
 Db 61 EALKANGVOVACLSYNDAFVTGEMGRHAKBGRKRLIADPTGAFGKETDILLDDSLVSI 120

RESULT 3
ABB11403
ID ABB11403 standard; peptide; 205 AA.

DT 11-JAN-2002 (first entry)

DE Human A1u co-repressor I homologue, SEQ ID NO:1773

Human, cytokine, cell proliferation; cell differentiation; growth factor
haematopoietic regulation; tissue growth; immunomodulator; activin
inhibin; chemokinesis; chemokinesis; thrombolytic; oncogenesis;
proliferation; metastasis; cancer; tumour; haematopoietic disorder;
myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
chronic inflammatory condition; proliferative retinopathy;
atherosclerosis; coronary heart disease; arterial ischaemia;
bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiaesthetic; antiarthritic; haemostatic; antiatherosclerotic;
cystostatic; osteopontic; vasostatic; cardiant; virucide; antibacterial;
antifungal; vulnery; anticancer.

Homo sapiens.

PN WO200157188-A2.

PD 09-AUG-2001

05-FEB-2001; 2001WO-US003800.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 P1
 XX WPI; 2001-457740/49.
 DR N-PSDB; ABA06647.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 PS
 XX Claim 20; Page 179; 1963pp; English.
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 CC
 XX
 SQ Sequence 205 AA;

Query Match 100.0%; Score 830; DB 4; Length 205;
 Best Local Similarity 100.0%; Pred. No. 6.9e-90;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEFEGEPGNKNVLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 60
 DB 44 MAPIKVGDALPAVEVEFEGEPGNKNVLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 103
 QY 61 EALKKAGVQVAACTSVNDAPFTGEMGRAHKAEGVRLADPTGAAGKGTDLILDLSLVS 120
 DB 104 EALKKAGVQVAACTSVNDAPFTGEMGRAHKAEGVRLADPTGAAGKGTDLILDLSLVS 163
 QY 121 FGNRLKRFMSVWVODGIYKALNVBPDGTGLTCSLAPNIISOL 162
 DB 164 FGNRLKRFMSVWVODGIYKALNVBPDGTGLTCSLAPNIISOL 205

RESULT 4

AAV17388
 ID AAV17388 standard; protein; 214 AA.
 XX
 AC AAV17388;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Human vesicle membrane protein-like protein 1.
 XX
 KM Human, vesicle membrane protein-like protein; VMP; Cushing's syndrome;
 KM developmental disorder; vesicle-trafficking disorder; cystic fibrosis;
 KM immunological disorder; reproductive disorder; neoplastic disorder;
 KM anaemia; muscular dystrophy; cataract; Grave's disease; allergy;
 KM ulcerative colitis; microbial infection; Addison's disease; cancer.
 XX
 OS Homo sapiens.
 XX
 PN W09921994-A2.
 XX
 PD 06-MAY-1999.
 XX
 PF 14-OCT-1998; 98WO-US021730.
 XX
 PR 28-OCT-1997; 97US-00959004.
 XX
 PA (INCY-) INCYTE PHARM INC.
 PI Hillman JL, Yue H, Corley NC, Lal P, Shah P;
 XX WPI; 1999-326702/27.
 DR N-PSDB; AAX56411.
 XX
 PT Human vesicle membrane-like proteins, useful for diagnosis, treatment and
 PT prevention of e.g. developmental disorders.
 XX
 PS Claim 1; Fig 1; 105pp; English.
 XX
 CC The present sequence represents human vesicle membrane protein-like
 CC protein 1 (VMP-1). VMP proteins, and their fragments, are used to treat
 CC or prevent developmental or vesicle-trafficking disorders, while their
 CC antagonists are used to treat or prevent immunological, reproductive or
 CC neoplastic disorders. Typical of many such disorders are anaemia;
 CC Cushing's syndrome; muscular dystrophy; cataract; cystic fibrosis;
 CC Grave's disease; ulcerative colitis; allergies; microbial infections;
 CC Addison's disease; cancer of breast, testis and prostate. VMP proteins
 CC are also used to raise specific antibodies (used to detect VMP in
 CC immunoassays (for diagnosis or monitoring), in competitive drug screens
 CC and to purify VMP from natural sources) and to screen for specific
 CC antagonists (potential therapeutic agents). VMP polynucleotides or their
 CC fragments, are used in hybridization assays to detect VMP in biological
 CC samples (e.g. for diagnosis, including detection of mutations and
 CC polymorphisms), optionally after amplification; to express recombinant
 CC VMP, including in vivo for gene therapy, and to map the corresponding
 CC genomic sequence
 CC
 XX
 SQ Sequence 214 AA;

Query Match 100.0%; Score 830; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 7.3e-90;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEFEGEPGNKNVLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 60
 DB 53 MAPIKVGDALPAVEVEFEGEPGNKNVLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 112
 QY 61 EALKKAGVQVAACTSVNDAPFTGEMGRAHKAEGVRLADPTGAAGKGTDLILDLSLVS 120
 DB 113 EALKKAGVQVAACTSVNDAPFTGEMGRAHKAEGVRLADPTGAAGKGTDLILDLSLVS 172
 QY 121 FGNRLKRFMSVWVODGIYKALNVBPDGTGLTCSLAPNIISOL 162
 DB 173 FGNRLKRFMSVWVODGIYKALNVBPDGTGLTCSLAPNIISOL 214

```
RESULT 5
ADJ68964
ID ADJ68964 standard; protein; 214 AA.
XX
XX ADJ68964;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human heat mitochondrial protein as a therapeutic target SeqID770.
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
XX Huntington's disease; osteoarthritis;
XX Leber's hereditary optic neuropathy; LHON;
XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarrhythmic;
XX osteopathic; ophthalmological; cytostatic.
XX
XX Homo sapiens.
XX
XX WO2003087768-A2.
XX
XX 23-OCT-2003.
XX
XX 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
XX 17-JUN-2002; 2002US-0389877P.
XX 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
XX (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX Warnock DE;
XX MPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
XX comprises detecting a modified polypeptide in a sample and correlating
XX with the disease.
XX
XX Claim 1; SEQ ID NO 770; 180bp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
XX for therapeutic intervention in treating a disease associated with
XX altered mitochondrial function. Specifically, it refers to a method for
XX identifying proteins of the human heart mitochondrial proteome that are
XX useful for drug screening assays, as well as therapeutic targets. The
XX present invention describes a method for identifying such proteins that
XX can be used in the treatment of various diseases associated with altered
XX mitochondrial function including diabetes mellitus, Huntington's disease,
XX osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX compositions have neuroprotective, nootropic, antidiabetic,
XX anticonvulsant, antiarrhythmic, osteopathic, ophthalmological and
XX cytostatic activities. This polypeptide sequence is a human heart
XX mitochondrial protein of the invention.
XX
XX Sequence 214 AA;
XX
XX Query Match 100.0%; Score 830; DB 7; Length 214;
XX Best Local Similarity 100.0%; Pred. No. 7.3e-90;
XX Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAPIKGDAIPAYVEEGEPGNKVNLAELFKGKGVLFVPGAFPTGCGSKTHLPGFVBOA 60
XX DB 53 MAPIKGDAIPAYVEEGEPGNKVNLAELFKGKGVLFVPGAFPTGCGSKTHLPGFVBOA 112
XX
XX 61 EALKAKGVQVAVCLSYNDAFVTGEMGRAHKAEGKRLADPTGAFGKETDLLLDDSLVSI 120
```

```
DB 113 EALKAKGVQVAVCLSYNDAFVTGEMGRAHKAEGKRLADPTGAFGKETDLLLDDSLVSI 172
XX
XX 121 FGNRLKRPSPWVQDGIYKALNVEPDGTCSLAPNIIISQL 162
XX DB 173 FGNRLKRPSPWVQDGIYKALNVEPDGTCSLAPNIIISQL 214
XX
XX RESULT 6
XX ADM83091
ID ADM83091 standard; protein; 214 AA.
XX
XX ADM83091;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human vesicle membrane protein (VMP)1.
XX
XX Vesicle membrane protein; VMP; cell proliferative disorder; cancer;
XX thyroid follicular adenoma; thyroid lymphocytic thyroiditis;
XX Crohn's disease; colon adenocarcinoma; breast papillomatosis;
XX breast adenocarcinoma; ovary serous papillary carcinoma;
XX ovary follicular cyst; cervix cervicitis;
XX uterus serous papillary carcinoma; uterus endometrial adenocarcinoma;
XX prostate adenofibromatous hyperplasia; prostate adenocarcinoma; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Region 28..49
XX FT /note= "Antigenic epitope"
XX FT Region 66..79
XX FT /note= "Antigenic epitope"
XX FT Region 174..182
XX FT /note= "Antigenic epitope"
XX FT Region 193..202
XX FT /note= "Antigenic epitope"
XX
XX US2003175787-A1.
XX
XX 18-SEP-2003.
XX
XX 19-MAR-2003; 2003US-00394136.
XX
XX 28-OCT-1997; 97US-00959004.
XX 22-NOV-2000; 2000US-00718996.
XX
XX (INCY-) INCYTE CORP.
XX
XX Hillman JL, Yue H, Lal P, Kaser MR;
XX PI
XX MPI; 2003-898530/82.
XX N-PSDB; ADM83146.
XX
XX New human vesicle membrane protein 1 (VMP1), useful for preparing a
XX PT composition for diagnosing, treating or preventing a disease or condition
XX associated with expression of VMP1 e.g., cancer.
XX
XX Claim 15; SEQ ID NO 1; 67bp; English.
XX
XX The present invention provides mammalian cDNAs which encode mammalian
XX vesicle membrane proteins (VMPs). The invention is useful for treating
XX conditions associated with decreased expression or overexpression of VMP1
XX such as cell proliferative disorders particularly cancers of the breast,
XX colon, ovary, uterus, prostate, adrenal gland and thyroid including
XX thyroid follicular adenoma, thyroid lymphocytic thyroiditis, Crohn's
XX disease, colon adenocarcinoma, breast papillomatosis, breast
XX adenocarcinoma, ovary serous papillary carcinoma, ovary follicular cysts,
XX cervix cervicitis, uterus serous papillary carcinoma, uterus endometrial
XX adenocarcinoma, prostate adenofibromatous hyperplasia and prostate
XX adenocarcinoma. The present sequence is human vesicle membrane protein
XX (VMP).
```

SQ Sequence 214 AA;
 Query Match 100.0%; Score 830; DB 7; Length 214;
 Best Local Similarity 100.0%; Pred. No. 7.3e-90;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPIKVGDAIPAVEVEFEGEPGNKVNLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 60
 DB 53 MAPIKVGDAIPAVEVEFEGEPGNKVNLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 112
 QY 61 EALRAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
 DB 113 EALRAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172
 QY 121 FGNRLKRFMSVWVDGIKALNVEPDGTGLTCSLAPNIISOL 162
 DB 173 FGNRLKRFMSVWVDGIKALNVEPDGTGLTCSLAPNIISOL 214
 RESULT 7
 ID ADM08846 standard; protein; 214 AA.
 AC ADM08846;
 AD 24-MAR-2005 (first entry)
 DE Human protein which is up-regulated in HCV-infected tissue - SEQ ID 183.
 KW gene targeting; hepatitis C virus infection; protein deactivation;
 KM protein activation.
 OS Homo sapiens.
 PN EP1493750-A2.
 PD 05-JAN-2005.
 PE 28-JUN-2004; 2004EP-00015098.
 PR 30-JUN-2003; 2003GB-00015248.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Berndt P, Kilby PM, Rugman P;
 WP1; 2005-050476/06.
 The invention relates to an antiviral compound having at least one down- and up-regulated hepatitis C virus (HCV) polypeptide, useful in predicting outcomes, treating or preventing HCV infections.
 Claim 1; SEQ ID NO 183; 346bp; English.
 The invention comprises the amino acid sequences of protein targets for anti-hepatitis C virus (anti-HCV) drugs. The human protein targets of the invention are either up-regulated or down-regulated in HCV-infected tissue. The proteins of the invention are useful in the preparation of a medicament for the treatment or prevention of HCV infection. The present amino acid sequence represents a human protein of the invention which is up-regulated in HCV-infected tissue.
 SQ Sequence 214 AA;
 Query Match 100.0%; Score 830; DB 9; Length 214;
 Best Local Similarity 100.0%; Pred. No. 7.3e-90;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPIKVGDAIPAVEVEFEGEPGNKVNLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 60
 DB 53 MAPIKVGDAIPAVEVEFEGEPGNKVNLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 112
 QY 61 EALRAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120

DB 113 EALRAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172
 QY 121 FGNRLKRFMSVWVDGIKALNVEPDGTGLTCSLAPNIISOL 162
 DB 173 FGNRLKRFMSVWVDGIKALNVEPDGTGLTCSLAPNIISOL 214
 RESULT 8
 ID ADY81123 standard; protein; 214 AA.
 AC ADY81123;
 AD 16-JUN-2005 (first entry)
 DE Human brain damage-related disorder marker, peroxiredoxin.
 KW diagnosis; neurological disease; neuroprotective; nootropic;
 KM Alzheimer's disease; Pick's disease; Parkinson's disease; degeneration;
 KM cerebroprotective; antiparkinsonian; peroxiredoxin.
 OS Homo sapiens.
 PN WO2005029088-A2.
 PD 31-MAR-2005.
 PE 20-SEP-2004; 2004WO-GB050012.
 PR 20-SEP-2003; 2003GB-00022063.
 PR 23-JUN-2004; 2004GB-00014089.
 PR 27-AUG-2004; 2004GB-00019068.
 PA (UYGE-) UNIV GENEVE.
 PA (LUCAS/) LUCAS B.
 PI Hochstrasser DF, Sanchez J, Lescuyer P, Allard L;
 WP1; 2005-242643/25.
 The invention relates to a method of diagnosing a brain damage-related disorder or its possibility in a subject suspected of suffering from it. The method is useful for diagnostic, prognostic and therapeutic applications relating to brain damage-related disorders. The method is useful for diagnosing a brain damage-related disorder such as cerebrovascular, dementia and neurodegenerative diseases, head trauma, CC ischemic stroke, hemorrhagic stroke, subarachnoid hemorrhage, intra cranial hemorrhage, transient ischemic attack, vascular dementia, CC Alzheimer's disease, Pick's disease, Parkinson's syndromes, CJD and other related disorders. The present sequence represents the amino acid sequence of a human brain damage-related disorder marker, peroxiredoxin.
 SQ Sequence 214 AA;
 Query Match 100.0%; Score 830; DB 9; Length 214;
 Best Local Similarity 100.0%; Pred. No. 7.3e-90;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPIKVGDAIPAVEVEFEGEPGNKVNLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 60
 DB 53 MAPIKVGDAIPAVEVEFEGEPGNKVNLAELFKGKKGVLFVGPAGFTPGSKTHLPGFVBOA 112
 QY 61 EALRAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120
 DB 113 EALRAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172

OY 121 FGNRLKRFMSVYVODGIYKALNVEPDGTGTCSLAPNIISQL 162
 DB 173 FGNRLKRFMSVYVODGIYKALNVEPDGTGTCSLAPNIISQL 214

RESULT 9
 AEA17061
 ID AEA17061 standard; protein; 214 AA.

AC AEA17061;

DT 11-AUG-2005 (first entry)

DE Alzheimer's disease associated protein #10.

KW neuroprotective; nootropic; gene therapy; neurodegenerative disorder;
 KW Alzheimer's disease; detection.

OS Homo sapiens.

PN US2005123962-A1.

PD 09-JUN-2005.

PF 26-OCT-2004; 2004US-00974148.

PR 28-OCT-2003; 2003US-0515536P.

(AGYT-) AGY THERAPEUTICS INC.

PI Gan L, Gonzalez-Zulueta M, Ye S, Uffer R, Nikolich K,

DR WPI: 2005-416976/42.

DR N-PSDB; AEA17060.

PT Detecting a (susceptibility to a) neurodegenerative disorder in a
 PT subject, comprises detecting differential expression of an Alzheimer's
 PT disease associated gene in a biological sample from the subject.

PS Claim 1; SEQ ID NO 20; 131pp; English.

XX The invention relates to a method of detecting neurodegenerative disorder
 CC or susceptibility to such a disorder in a subject in a sample from the
 CC subject differential expression of a gene encoding a polypeptide
 CC comprising a linear sequence of at least 8 amino acids, which is
 CC essentially identical to a contiguous fragment of 8 amino acids found in
 CC any of SEQ ID Nos 2-54 (even SEQ ID Nos) . (M1) is useful for detecting a
 CC neurodegenerative disorder or susceptibility to a neurodegenerative
 CC disorder in a subject. The neurodegenerative disorder is characterized by
 CC a property chosen from neuronal loss, amyloid Abgr; plaque formation,
 CC mononuclear phagocyte activation and mononuclear phagocyte neurotoxicity,
 CC where the neurodegenerative disorder is Alzheimer's disease. This
 CC sequence corresponds to a differentially expressed protein detected by
 CC the method of the invention.

XX Sequence 214 AA;

Query Match 100.0%; Score 830; DB 9; Length 214;
 Best Local Similarity 100.0%; Pred. No. 7,3e-90;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAPITKGDAIPAVEVEGEPGNKVNLAELFKGKGVLPFGPAGFTPGCSKTHLPGFVEOA 60

DB 53 MAPITKGDAIPAVEVEGEPGNKVNLAELFKGKGVLPFGPAGFTPGCSKTHLPGFVEOA 112

OY 61 EALKAGVQVAVLSTVNDAPVTGEMGRANKAEKGVLLADPTGAFKERTDLLDLSLVS1 120

DB 113 EALKAGVQVAVLSTVNDAPVTGEMGRANKAEKGVLLADPTGAFKERTDLLDLSLVS1 172

OY 121 FGNRLKRFMSVYVODGIYKALNVEPDGTGTCSLAPNIISQL 162

DB 173 FGNRLKRFMSVYVODGIYKALNVEPDGTGTCSLAPNIISQL 214

RESULT 10

ID ADJ70591
 ID ADJ70591 standard; protein; 161 AA.

AC ADJ70591;

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID2397.

KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.

OS Homo sapiens.

PN WO2003087768-A2.

PD 23-OCT-2003.

PF 04-APR-2003; 2003WO-US010870.

PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-038987P.

PR 20-SEP-2002; 2002US-0412418P.

PA (MITO-) MITOKOR.

PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM,

DR WPI: 2003-845369/78.

PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.

PS Claim 1; SEQ ID NO 2397; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

XX Sequence 161 AA;

Query Match 99.4%; Score 825; DB 7; Length 161;
 Best Local Similarity 100.0%; Pred. No. 1.9e-89;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APIKYGDAIPAVEVEGEPGNKVNLAELFKGKGVLPFGPAGFTPGCSKTHLPGFVEOA 61

DB 1 APIKYGDAIPAVEVEGEPGNKVNLAELFKGKGVLPFGPAGFTPGCSKTHLPGFVEOA 60

Query Match 93.6%; Score 777; DB 5; Length 226;
 Best Local Similarity 95.1%; Pred. No. 1.6e-83;
 Matches 154; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGGVLFVPGAFPTPGSKTHLPGFVEQA 60
 DB 52 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGGVLFVPGAFPTPGSKTHLPGFVEQA 111
 QY 61 EALKAKGVQVVAACLSVNDAFVTGEMGRAHKAEGVRLADPTGAFGKETDILLDDSLVSI 120
 DB 112 EALKAKGVQVVAACLSVNDAFVTGEMGRAHKAEGVRLADPTGAFGKETDILLDDSLVSI 171
 QY 121 FGNRLKRFPSMVVQDGIYKALNVEPDGTGLTCSLAPNIISQL 162
 DB 172 FGNRLKRFPSMVVQDGIYKALNVEPDGTGLTCSLAPNIISQL 213

RESULT 13
 ABU00319
 ID ABU00319 standard; protein; 194 AA.
 XX
 AC ABU00319;

DT 17-JAN-2003 (first entry)
 XX
 DE Human novel polypeptide #412.

XX Human; genetic disorder; gene mapping; medical imaging; cancer;
 XX neurodegenerative disorder; lymphoid cell disorder; osteoporosis;
 XX Parkinson's disease; Alzheimer's disease; bone degenerative disorder;
 XX osteoarthritis; peridontal disease; liver fibrosis; viral infection;
 XX fungal infection; bacterial infection; autoimmune disease; diabetes;
 XX atopic dermatitis.

OS Homo sapiens.
 XX
 PN WO200274961-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 14-MAR-2002; 2002WO-US005109.
 XX
 PR 15-MAR-2001; 2001US-00810173.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehman T, Wang J, Wang D, Drmanac RT;

XX WPI; 2003-040556/03.
 DR N-PSDB; ABX05397.

PT New isolated polypeptides and polynucleotides, useful for preventing,
 PT treating or ameliorating medical conditions, such as cancer,
 PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative
 PT disorders, and infections.

PS Claim 9; SEQ ID NO 938; 235pp; English.

XX The invention relates to human polynucleotides and the polypeptides they
 CC encode. The polynucleotides and polypeptides are useful in diagnostics,
 CC forensics, gene mapping, medical imaging, identification of mutations,
 CC responsible for genetic disorders or other traits, assessing biodiversity
 CC and producing many other types of data and products dependent on DNA and
 CC amino acid sequences. They are also useful for preventing, treating or
 CC ameliorating medical conditions, such as cancer, neurodegenerative
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell
 CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,
 CC peridontal disease, liver fibrosis, infections (e.g. viral, fungal or
 CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).
 CC Sequences ABG9388-ABG9389 and ABU0010-ABU00433 represent human
 CC polypeptides of the invention. Note: The sequence data for this patent is

CC not represented in the printed specification but is based on sequence
 CC information supplied by the European Patent Office

XX Sequence 194 AA;

QY Query Match 84.5%; Score 701; DB 6; Length 194;
 DB Best Local Similarity 87.7%; Pred. No. 1.5e-74;
 XX Matches 142; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGGVLFVPGAFPTPGSKTHLPGFVEQA 60
 DB 53 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGGVLFVPGAFPTPGSKTHLPGFVEQA 112
 QY 61 EALKAKGVQVVAACLSVNDAFVTGEMGRAHKAEGVRLADPTGAFGKETDILLDDSLVSI 120
 DB 113 EALKAKGVQVVAACLSVNDAFV-----TGAFGKETDILLDDSLVSI 152

QY 121 FGNRLKRFPSMVVQDGIYKALNVEPDGTGLTCSLAPNIISQL 162
 DB 153 FGNRLKRFPSMVVQDGIYKALNVEPDGTGLTCSLAPNIISQL 194

RESULT 14
 AAB87638
 ID AAB87638 standard; protein; 150 AA.
 XX
 AC AAB87638;

DT 15-MAY-2001 (first entry)

XX Bovine mammary tissue derived protein #29.

XX Bovine; mammary gland; cancer; tumour; angiogenesis.

OS Bos taurus.
 XX
 PN WO200114553-A1.
 XX
 PD 01-MAR-2001.
 XX
 PF 23-AUG-2000; 2000WO-NZ000166.
 XX
 PR 23-AUG-1999; 99US-0150330P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
 PI Havukkala IJ, Gleen M, Grigor MR, Molenaar AJ;

XX WPI; 2001-226619/23.

PT New polypeptides and polynucleotides encoding the polypeptides, which are
 PT expressed in bovine mammary gland tissue, useful for stimulating mammary
 PT gland growth or function, or inducing differentiation of milk producing
 PT cells.

PS Claim 11; Page 72; 97pp; English.

XX The present invention relates to proteins derived from bovine mammary
 CC gland cells. The invention is useful for stimulating bovine mammary gland
 CC cell growth and function, inhibiting the growth of various mammary gland
 CC cancer cells, inhibiting angiogenesis and vascularization of tumours, or
 CC modulating the growth of blood vessels in a mammal

XX Sequence 150 AA;

QY Query Match 80.4%; Score 667; DB 4; Length 150;
 DB Best Local Similarity 87.0%; Pred. No. 1.1e-70;
 XX Matches 127; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGGVLFVPGAFPTPGSKTHLPGFVEQA 60
 DB 5 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGGVLFVPGAFPTPGSKTHLPGFVEQA 64

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:42:32 ; Search time 39 Seconds
(without alignments)
399.670 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPIKVGDALPAVEFEGEP.....VEPDGTGLTSLAPNIISQL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630.5	76.0	209	2	peroxiredoxin V -
2	317	38.2	191	2	AB3434
3	312.5	37.7	160	2	AbpC/ISA family pr
4	303	36.5	161	2	hypothetical prote
5	303	36.5	161	2	peroxiredoxin [imp
6	297.5	35.8	157	2	probable antioxidant
7	294	35.4	162	2	B96684
8	289.5	34.9	234	2	T47553
9	286	34.5	162	2	A96684
10	275.5	33.2	251	2	AG1998
11	252.5	30.4	189	2	S74815
12	250.5	30.2	245	2	G81140
13	243.5	29.3	247	2	D82051
14	225.5	27.2	243	2	AB0477
15	219.5	26.4	241	2	I64154
16	219	26.4	178	2	AG2871
17	219	26.4	212	2	G97647
18	216	26.0	156	2	T41316
19	213.5	25.7	167	2	A33646
20	210	25.3	553	2	D96684
21	209.5	25.2	179	2	S35907
22	208.5	25.1	167	2	B36646
23	194	23.4	164	2	G96632
24	191.5	23.1	166	2	JR0227
25	191	23.0	177	2	JR0226
26	147	17.7	176	2	S64946
27	115	13.9	195	2	T39667
28	114.5	13.8	215	2	S74033
29	114	13.7	218	2	S60285

30	109	13.1	187	2	A86667	alkyl hydroperoxid
31	108	13.0	211	2	G70343	alkyl hydroperoxid
32	107.5	13.0	215	2	H72330	hypothetical prote
33	107.5	13.0	222	2	H64391	alkyl hydroperoxid
34	107	12.9	168	2	B80179	hypothetical prote
35	107	12.9	187	2	D90709	alkyl hydroperoxid
36	107	12.9	187	2	H85559	alkyl hydroperoxid
37	107	12.9	187	2	JN0289	alkyl hydroperoxid
38	104.5	12.6	207	2	B82287	antioxidant, AbpC/
39	104	12.5	187	2	AB0577	antioxidant, AbpC/
40	102.5	12.3	153	2	AH2203	bacterioferritin c
41	102.5	12.3	157	2	AG0372	bacterioferritin c
42	101.5	12.2	220	2	T03967	RAB24 protein - r1
43	101	12.2	216	2	C75081	probable peroxid
44	101	12.2	216	2	C71065	probable alkyl hyd
45	98.5	11.9	250	2	B72454	probable thioredox

ALIGNMENTS

RESULT 1

UC7239
peroxiredoxin V - mouse

C:Species: Mus musculus (house mouse)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C:Accession: UC7239
R:Lee, T.H.; Kim, S.J.; Kang, S.W.; Lee, K.K.; Rhee, S.G.; Yu, D.Y.

Biochem. Biophys. Res. Commun. 270, 356-362, 2000
A:Title: Molecular cloning and characterization of the mouse peroxiredoxin V gene.

A:Reference number: JC7239
A:Accession: UC7239
A:Molecule type: mRNA

A:Residues: 1-209 <LBR>
A:Cross-references: UNIPROT:P99029; UNIPARC:UPI000016C928; GB:AF208729

A:Experimental source: liver
A:Comment: This protein, thiol-specific antioxidant, belonging to peroxiredoxin family,

peroxides, and influences the differentiation, proliferation, activity and survival of C:Genetics:

A:Gene: Prxv

A:Map position: 19

A:introns: 53/3; 98/2; 141/3; 154/3; 175/2
C:Keywords: liver

Query Match 76.0%; Score 630.5; DB 2; Length 209;

Best local similarity 78.0%; Pred. No. 6.1e-51;
Matches 131; Conservative 6; Mismatches 18; Indels 13; Gaps 2;

QY	1	MAPIKVGDALPAVEFEGEPGNKYNLAELFKGKGVLFVGPAGFTPGCSKTHL-----P	54
DB	49	MAPIKVGDALPAVEFEGEPGNKYNLAELFKGKGVLFVGPAGFTPGCSKTHL-----P	101
QY	55	GFVQAEALAKKAGQVVAACISVNDAPVTGEMGRARHAKGKVRLLADPTGAFKGTDLILD	114
DB	102	GFVQAGALAKKAGQVVAACISVNDAPVTGEMGRARHAKGKVRLLADPTGAFKGTDLILD	161
QY	115	DSVSIKGNRRLKRSWVODGIVKALNVEDGKGLTCSLAPNIISQL	162
DB	162	DSVSIKGNRRLKRSWVODGIVKALNVEDGKGLTCSLAPNIISQL	209

RESULT 2

AB3434
thiol peroxidase (EC 1.11.1.-) [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: AB3434
R:DeVeechio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688
A:Accession: AB3434

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <KUR>
A:Cross-references: UNIPROT:Q8YF4; UNIPARC:UP10000058096; GB:AE008917; PIDN:AA152637.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11456
A:Map position: 1
C:Keywords: oxidoreductase

Query Match 38.2%; Score 317; DB 2; Length 191;
Best Local Similarity 42.9%; Pred. No. 5.3e-22;
Matches 69; Conservative 30; Mismatches 58; Indels 4; Gaps 2;
QY 4 IKVGDAIPAV--EVEFGEBCNKVNLAELFKGKGVLPFGVGAFTPGCKSTHLPGEVQAE 61
DB 33 IKVGDTLPATFETVTAGDGTETTTDDVFKGRKVLFAVPGAFPTCSLNHLPGYLENRD 92
QY 62 ALKAGVQVACLSVNDAPVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIF 121
DB 93 AILAKGVDDIAVAVNDPVMGMAQSTGSEKILFLADGSAFTTGAAGLIDLDLSSGGL- 151
QY 122 GNRRLKRFPSMVVQDGIKALNVEPDGTGLTCSLAPNIISQL 162
DB 152 -GVRSKRYSMLVEDGVKSLNTEBPQGAFTVSAALAEQL 191

RESULT 3

h87668
AmpC/TSA family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87669
R.Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Grimm, M.L.; Haft, D.H.; Kojan
n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87669
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <STO>
A:Cross-references: UNIPROT:Q9A312; UNIPARC:UP100000C7A6D; GB:AE005673; NID:G13425104; F
C:Genetics:
A:Gene: CC3394

Query Match 37.7%; Score 312.5; DB 2; Length 160;
Best Local Similarity 45.1%; Pred. No. 1.1e-21;
Matches 73; Conservative 21; Mismatches 61; Indels 7; Gaps 4;
QY 4 IKVGDAIPAVEV--EGEGGNKNLAELFKGKGVLPFGVGAFTPGCKSTHLPGEVQAE 61
DB 3 IKVGDTLPATFETVTAGDGTETTTDDVFKGRKVLFAVPGAFPTCSLNHLPGFEKAD 62
QY 62 ALKAGVQVACLSVNDAPVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIF 121
DB 63 ELKAKGVDDIVCSVNDVVMKMGMDQGDSEVLLIADGNGDFTKALIGLDPDGSK---F 119
QY 122 G-NRRLKRFPSMVVQDGIKALNVEPDGTGLTCSLAPNIISQL 162
DB 120 GNGARSGRYSMLVEDGVKSLNTEBPQGAFTVSAALAEQL 160

RESULT 4

C97454
Hypothetical protein AGR_C1423 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: C97454
R.Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wolian, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappae, C.; Markelz, B.;
Science 294, 2333-2338, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: C97454
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-161 <KUR>
A:Cross-references: UNIPROT:Q8UHA4; UNIPARC:UP100000D1911; GB:AE007869; PIDN:AAK86588.1;
C:Genetics:
A:Gene: AGR_C1423
A:Map position: circular chromosome

Query Match 36.5%; Score 303; DB 2; Length 161;
Best Local Similarity 44.7%; Pred. No. 8.5e-21;
Matches 72; Conservative 22; Mismatches 63; Indels 4; Gaps 2;
QY 4 IKVGDAIPAVEVFESEPGNKVNLA--ELFKGKGVLPFGVGAFTPGCKSTHLPGEVQAE 61
DB 3 IKIGKLSATFETKETAADGPEVETTTDALFGKRVLPFAVPGAFPTCSLNHLPGYLENRD 62
QY 62 ALKAGVQVACLSVNDAPVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIF 121
DB 63 AILAKGVDDIAVSVNDHVMGMAQSSGCGCKIHFLADWDASFTKA--LGILDADLSGGG 120
QY 122 GNRRLKRFPSMVVQDGIKALNVEPDGTGLTCSLAPNIISQL 162
DB 121 LGVRSKRYSMLVEDGVKSLNTEBPQGAFTVSAALAEQL 161

RESULT 5

AE2672
peroxiredoxin [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE2672
R.Wood, D.W.; Setubal, J.C.; Kaul, R.; Marks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, L
erage, G.; Gillet, W.; Grant, C.; Gendhner, D.; Kutyavlin, T.; Levy, R.; Li, M.; McEllell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tso, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AE2577; MUID:21608550; PMID:11743193
A:Accession: AE2672
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-161 <KUR>
A:Cross-references: UNIPROT:Q8UHA4; UNIPARC:UP100000D1911; GB:AE008688; PIDN:AA1795.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0779
A:Map position: circular chromosome

Query Match 36.5%; Score 303; DB 2; Length 161;
Best Local Similarity 44.7%; Pred. No. 8.5e-21;
Matches 72; Conservative 22; Mismatches 63; Indels 4; Gaps 2;
QY 4 IKVGDAIPAVEVFESEPGNKVNLA--ELFKGKGVLPFGVGAFTPGCKSTHLPGEVQAE 61
DB 3 IKIGKLSATFETKETAADGPEVETTTDALFGKRVLPFAVPGAFPTCSLNHLPGYLENRD 62
QY 62 ALKAGVQVACLSVNDAPVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSIF 121
DB 63 AILAKGVDDIAVSVNDHVMGMAQSSGCGCKIHFLADWDASFTKA--LGILDADLSGGG 120
QY 122 GNRRLKRFPSMVVQDGIKALNVEPDGTGLTCSLAPNIISQL 162
DB 121 LGVRSKRYSMLVEDGVKSLNTEBPQGAFTVSAALAEQL 161

RESULT 6

DB2209
probable antioxidant VC1350 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae

```

Qy      58 EQAEALAKAGVAVACTSVNDAAFTGEMGRAHKAEGKRYLLADPTGAF----GKETDLL 113
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 EKAEELSKSGVDEILICFSVNDPVMKAMGKTYENKHYKFAVDAGSGEYTHLLGIELD--L 118

```

Query Match	34.5%	Score 286	DB 2	Length 162
Best Local Similarity	40.2%	Pred. NO. 3.2e-19		
Matches 68; Conservative	29	Mismatches 38	Indels 14	Gaps 6

Oy MAPLKYGAIP--ANEVF-EGEPGNKYNLAIEFGKKVLTGVPAPFPGSGKTHLPGFV 57
| | | | | :
Db 1 MAPIIVGVNVDPGRTISFPDENDDQLOTVSVSHI5IAAGKYLILGVPALPPTCSMSHVPGEI 60
| | | | | :
Oy 58 EOAEALKAKGVQVAVCLSVNDAFYVTGEWGRAHKAGKVRLADPTGAF---GKRTDLLL 113
| : | : | :
Db 61 GKAEELTKSGKIDIELICFSVDNPFWKAWKGCTYPERKHVKFPAVDGSGEYTHLLGLDEL-L 118
| : | : | : | :
Oy 114 DDSLVSTIGNRRLKRFSNWODGIYKALANVEPDGTLTCSLAPNISQL 162
| : | : | : | : | :
Db 119 KDKGLGI---RSRRFALLDLNLKVTANVESGGF-FTVSABEDILKAL 162
| : | : | : | : | :

RESULT 10
AG1998
peroxidodoxin 2 family protein/glutaredoxin [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Nnote: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #strain PCC 7120 #text_change 09-Jul-2004
C:Accession: AG1998
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchih
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG1998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <KUB>
A:Cross-references: UNIPROT:O8YWR3; UNIPARC:UP100000CEB11; GB:BA000019; PIDN:BAB77907.1
A:Experimental source: strain PCC 7120
C:Genetics:
C:Gene: all1541

Query Match	33.2%	Score 275.5	DB 2	Length 251
Best Local Similarity	41.1%	Pred. No. 5,1e-18		
Matches	60	Conservative 27	Mismatches 52	Indels 7
			Gaps 5	
Qy	7	GDATPAVAVFPECEPENK---	VNLALFPGKKGVLPGVGAFFPGCSKTHLPGEQAEAL	63
		: : : : : : :	: : : : : : :	
Db	7	GORVQV--TFKTRONNEWVNTTDDL	FMAGKTVAVASFLSCGATTPYCSSLHFGYIELAKVF	65
		: : : : : : :	: : : : : : :	
Qy	64	RAKGVQVAVACTSVNDAPVTGEMGRARHKAEGKRVLLADPTGA	FGKETDLLLLDSLVSIIFGN	123
		: : : : : : :	: : : : : : :	
Db	66	KONGVDIELICTSVNDAPFVNIENAKTQBAE--NITLLPDNGEFTBGMGLVDTKDILG--FG-		122
		: : : : : : :	: : : : : : :	
Qy	124	RLRKFSFNVVQDGIYKALNVEPDGTG		149
		: : : : : : :	: : : : : : :	
Db	123	KRSWRYSLVYKDGVTLEKMFIEBDVPG		148
		: : : : : : :	: : : : : : :	

```

RESULT 11
S74815
membrane protein - Synechocystis sp. (strain PCC 6803)
N/Alternate names: protein sll1621
C/Species: Synechocystis sp.
A/Variety: PCC 6803
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S74815
R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O., K.; Okumura, S.; Shilpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A/Reference number: S74322; MUID:97061201, PMID:8905231
A/Accession: S74815
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-189 <KAN>
A/Cross-references: UNIPROT:P73728; UNIPARC:UPI000013A3E; EMBL:D90909; GB:AB001339; NITR
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      30.4%; Score 252.5; DB 2; Length 189;

```

Best Local Similarity 39.8%, Pred. No. 4.8e-16; Matches 64; Conservative 27; Mismatch 53; Indels 17; Gaps 7;

RESULT 12

GB1140

peroxiredoxin 2 family protein/glutaredoxin NMB0946 [imported] - *Neisseria meningitidis*

C|Species: *Neisseria meningitidis*

C|Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

A|Accession: GB1140; H81880

R|Retcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Jin, H.; Vamthepan, V.; Gill, J.; Scariato, V.; Masiugani, V.; Pizarra, M.

A|Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoli, R.; V

A|Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A|Reference number: AB1000; MUID:20175755; PMID:10710307

A|Accession: GB1140

A|Status: Preliminary

A|Molecule type: DNA

A|Residues: 1-245 <TEP>

A|Cross-references: UNIPROT:O9JOS4; UNIPARC:UPI00000C4B6C; GB:AE002445; GB:AE002098; NIT

A|Experimental source: serogroup B, strain MC58

R|Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

|; Holtz, S.; Jorgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream

A|Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A|Reference number: AB1775; MUID:20222556; PMID:10761919

A|Accession: H81880

A|Status: Preliminary

A|Molecule type: DNA

A|Residues: 1-245 <PAR>

A|Cross-references: UNIPARC:UPI00000C4B6C; GB:AL162755; GB:AL157959; NID:G7379742; PIDN

A|Experimental source: serogroup A, strain Z2491

C|Genetics:

A|Gene: NMB0946; NMA1141

```

Query March 30.2%; Score 250.5; DB 2; Length 245;
Best Local Similarity 38.5%; Pred. NO. 1e-15;
Matches 57; Conservative 28; Mismatches 56; Indels 7; Gaps 5;

QY KVGDAIPAVEVEE--GEPGNKVLAELFKGKKGVLPFGPAFTPGCSKTHLPGEVQAE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  RTGGKVPSPV-VFRTRVGDPWMDVSTDDLFGKKKVVVPSLPGAFPTCSSSHLPYNEILFG 64

QY ALKAKGVAVACLSVNDAPFTGEGRAHKAEGKRLADLPFGAGCKETDLIDSLYSIF 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  AFGKNGDAIACVSVNDTFVNNANA-AEESDNITYIPDGNGEFTEGGMVLGKEDLG-F 122

QY GNRLKRFPSMVVDGIVKALNVBPDGTG 149
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  G-KRSMRYSLMVDGVEKMFIEPEBFG 149

RESULT 13
DB2051
peroxiredoxin family protein/glutaredoxin VC2637 [Imported] - Vibrio cholerae (strain N1696)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: DB2051
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

```